

90489

From: Chan, Christina  
Sent: Tuesday, April 01, 2003 12:31 PM  
To: Rao, Manjunath N.; STIC-Biotech/ChemLib  
Subject: RE: Request for RUSH sequence search for 09/595526

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

RECEIVED  
APR - 1 2003  
(STIC)

-----Original Message-----

From: Rao, Manjunath N.  
Sent: Tuesday, April 01, 2003 12:29 PM  
To: Chan, Christina  
Subject: Request for RUSH sequence search for 09/595526

Hello Christina,

Please authorize the request below as RUSH. The reason being ~~this case~~ is due soon and applicants have changed the sequence claims.

Thanks  
Manjunath

10D01

From: Manjunath N. Rao ← deliver to  
Art Unit 1652, Room 10A11  
Mail Box in Room 10C 01?  
Phone: 306-5681

Point of Contact:  
Barb O'Bryen  
Technical Information Specialist  
STIC CM1 6A05 308-4291

Date: 4-1-03

Please search the following as soon as possible for application with serial number  
**09/595,526 (Update)**

1. Nucleotides 1-500, 2250-2750, 4750-5250, 7250-7750, 9500-10,276 of SEQ ID NO:1  
(total number of nucleotides to be searched= 2726)

Searcher: MBB  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 4-4-03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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90489

2. Nucleotides 291-7074 of SEQ ID NO:1 (total number of nucleotides=6784)

against all commercial nucleic acid databases including issued patents database and pending application database and provide a **print of all results**.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D.  
Biotechnology Patent Examiner  
Art Unit 1652, Room 10A11  
Crystal Mall 1, USPTO.

RECEIVED  
APR - 1 2003  
(STIC)

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
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TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
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Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 990.903 Seconds  
(without alignments)  
14684.987 Million cell updates/sec

Title: US-09-595-526c-1\_COPY\_1\_500

Perfect score: 500

Sequence: 1 ggcgggaccgcagagccg.....cagaacattccttggtt 500

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_pl.\*  
8: gb\_pr.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
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13: gb\_vt.\*  
14: gb\_vt.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
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20: em\_om.\*  
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22: em\_ov.\*  
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26: em\_ro.\*  
27: em\_sts.\*  
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29: em\_vt.\*  
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31: em\_hig\_inv.\*  
32: em\_hig\_other.\*  
33: em\_hig\_mus.\*  
34: em\_hig\_pln.\*  
35: em\_hig\_rtd.\*  
36: em\_hig\_vrt.\*  
37: em\_hig\_vrt.\*  
38: em\_sv.\*  
39: em\_higo\_hum.\*  
40: em\_higo\_mus.\*  
41: em\_higo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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| 3          | 500   | 100.0 | 10442  | 9  | AF285167   | Homo sapi   |
| 4          | 492.6 | 98.5  | 10474  | 6  | AX060719   | Sequence    |
| 5          | 492.6 | 98.5  | 10474  | 6  | AX060721   | Sequence    |
| 6          | 492.6 | 98.5  | 10474  | 6  | AX060898   | Sequence    |
| 7          | 492.6 | 98.5  | 10474  | 6  | AX060900   | Sequence    |
| 8          | 486.4 | 97.3  | 7260   | 6  | AX253452   | Sequence    |
| 9          | 484.4 | 96.9  | 697    | 9  | AF258627   | Homo sapi   |
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| 11         | 483.2 | 96.6  | 9854   | 6  | AX139818   | Sequence    |
| 12         | 481.6 | 96.3  | 1556   | 9  | AX024328   | Homo sapi   |
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| 14         | 378.2 | 75.6  | 446    | 6  | AX137751   | Sequence    |
| 15         | 378.2 | 75.6  | 9741   | 6  | AX127830   | Sequence    |
| 16         | 378.2 | 75.6  | 9741   | 6  | AX139817   | Sequence    |
| 17         | 378.2 | 75.6  | 9741   | 6  | AX351038   | Sequence    |
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| 33         | 197   | 39.4  | 221    | 6  | AX351032   | Sequence    |
| 34         | 195.6 | 39.1  | 7878   | 10 | MMAB01     | Mus musculu |
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# ALIGNMENTS

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

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Sequence 1 from Patent WO0078972.  
AX060713  
AX060713.1 GI:12406103  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10442)  
Lawn,R.W., Wade,D. and Garvin,M.  
Regulation with binding cassette transporter protein abcl  
Patent: WO 0078972-A 1 28-DEC-2000;

AX060713  
Sequence 1 from Patent WO0078972.  
AX060713  
AX060713.1 GI:12406103  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10442)  
Lawn,R.W., Wade,D. and Garvin,M.  
Regulation with binding cassette transporter protein abcl  
Patent: WO 0078972-A 1 28-DEC-2000;

AX060713  
Sequence 1 from Patent WO0078972.  
AX060713  
AX060713.1 GI:12406103  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10442)  
Lawn,R.W., Wade,D. and Garvin,M.  
Regulation with binding cassette transporter protein abcl  
Patent: WO 0078972-A 1 28-DEC-2000;

Pred. No. is the number of results predicted by chance to have a



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Query Match 100.0%; Score 500; DB 9; Length 10442;  
Best Local Similarity 100.0%; Pred. No. 1,2e-134;  
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DB 1 GGCGGGACCCGAGAGCCGACCCCTCTCTCCCGGGCTGCGGAGGCGGCGG 60  
QY 61 GGAGCTCCGGCACCACAGAGCCGCTTCTCAGGCGCTTCTCTCTCTCTCTCT 120  
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QY 121 GTTCTGTTTCT 180  
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QY 181 ACAAAGTGGAAACAGTAAATGACACAGCCAGGGGCTGCTGCTGCTGCTGCTGCT 240  
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LOCUS  
DEFINITION Sequence 7 from Patent WO0078972.  
ACCESSION AX060719  
VERSION AX060719.1 GI:12406108  
KEYWORDS  
human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10474)  
AUTHORS Lawn, R.M., Wade, D. and Garvin, M.  
TITLE Regulation with binding cassette transporter protein abel  
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
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DEFINITION Sequence 9 from Patent WO0078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
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Best Local Similarity 99.2%; Pred. No. 1.8e-132;
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QY 2 GCCGGGACCCGAGAGCCGAGCCGCTTCTCTCCGGGCTCGCGCAGGGCAGGGCGGG 61
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QY 482 AGGAACACTTCTTGGGTT 500
Db 514 AGGAACACTTCTTGGGTT 532

RESULT 6
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LOCUS AX060721 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 9 from Patent WO0078972.
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abcl
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source
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BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
ORIGIN
Query Match 98.5%; Score 492.6; DB 6; Length 10474;
Best Local Similarity 99.2%; Pred. No. 1.8e-132;
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GCCGGGACCCGAGAGCCGAGCCGCTTCTCTCCGGGCTCGCGCAGGGCAGGGCGGG 61
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Db 514 AGGAACACTTCTTGGGTT 532

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AX060898
LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078971.
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
Location/Qualifiers
source
1..10474
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
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Query Match 98.5%; Score 492.6; DB 6; Length 10474;
Best Local Similarity 99.2%; Pred. No. 1.8e-132;
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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LOCUS AX060900 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 9 from Patent WO0078971.
ACCESSION AX060900
VERSION AX060900.1 GI:12406276
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 10474)  
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.  
TITLE Atp binding cassette transporter protein abcl polypeptides  
JOURNAL Patent: WO 0078971-A 9 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
FEATURES Location/Qualifiers  
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AX253452 7260 bp DNA linear PAT 10-OCT-2001  
LOCUS Sequence 3 from Patent WO0170810.  
DEFINITION AX253452  
ACCESSION AX253452.1 GI:16073979  
VERSION  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 7260)  
AUTHORS Schmitz, G. and Bodzioch, M.  
TITLE Atp binding cassette transporter 1 (abcl) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders  
JOURNAL Patent: WO 0170810-A 3 27-SEP-2001;  
Bayer Aktiengesellschaft (DE)  
FEATURES Location/Qualifiers

source 1..7260  
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BASE COUNT 1834 a 1765 c 1905 g 1756 t  
ORIGIN /db\_xref="taxon:9606"  
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Best Local Similarity 99.6%; Pred. No. 1.1e-130;  
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DEFINITION partial cds.  
ACCESSION AF258627  
VERSION  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 697)  
AUTHORS Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.  
TITLE Analysis of hABCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms  
JOURNAL Biochem. Biophys. Res. Commun. 271 (2000) In press  
REFERENCE 2 (bases 1 to 697)  
AUTHORS Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.  
TITLE Direct Submission  
JOURNAL Submitted (19-APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA  
FEATURES Location/Qualifiers

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Best Local Similarity 99.2%; Pred. No. 3.5e-130;
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RESULT 10
AX127831
LOCUS AX127831
DEFINITION Sequence 70 from Patent W00130848.
ACCESSION AX127831
VERSION AX127831.1 GI:14134478
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9854)
AUTHORS Deneffe,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abci gene and their therapeutic and
diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 2665 a 2219 c 2334 g 2635 t 1 others
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Query Match 96.6%; Score 483.2; DB 6; Length 9854;
Best Local Similarity 99.2%; Pred. No. 9.8e-130;
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RESULT 11
AX139818
LOCUS AX139818
DEFINITION Sequence 70 from Patent EP1096012.
ACCESSION AX139818
VERSION AX139818.1 GI:14275400
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9854)
AUTHORS Deneffe,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,I.I.,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abci gene and their therapeutic and
diagnostic application

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JOURNAL Patent: EP 1096012-A 70 02-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
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LOCUS
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to ATP-BINDING CASSETTE TRANSPORTER 1.
ACCESSION AK024328
VERSION AK024328.1 G:10436685
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE1
clone:PLACE1002437.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiyasu,S., Komai,F., Hara,R., Takeuchi,K.,
Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.
NEDO human cDNA sequencing project
Unpublished
JOURNAL 2 (bases 1 to 1556)
REFERENCE Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection;
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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DEFINITION Sequence 3 from Patent WO0130848.
ACCESSION AXI27764
VERSION AXI27764.1 GI:14134411
KEYWORDS
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ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 446)
AUTHORS
Densfle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
TITLE
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL
Patent: WO 0130848-A 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
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/db_xref="taxon:32630"
/Note="Oligonucleotide Primer"
BASE COUNT 96 a 123 c 112 g 115 t
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Best Local Similarity 99.0%; Pred. No. 3.2e-99;
Matches 391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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ACCESSION AXI139751
VERSION AXI139751.1 GI:14275333
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 446)
AUTHORS
Densfle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
TITLE
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL
Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
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Location/Qualifiers
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BASE COUNT 2650 a 2180 c 2290 g 2620 t
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TITLE
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/Note="Oligonucleotide Primer"
BASE COUNT 96 a 123 c 112 g 115 t
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Query Match 75.6%; Score 378.2; DB 6; Length 446;
Best Local Similarity 99.0%; Pred. No. 3.2e-99;
Matches 391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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RESULT 15
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LOCUS
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ACCESSION AXI27830
VERSION AXI27830.1 GI:14134477
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 9741)
AUTHORS
Densfle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
TITLE
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL
Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2650 a 2180 c 2290 g 2620 t
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Query Match      75.6%; Score 378.2; DB 6; Length 9741;
Best Local Similarity 99.0%; Pred. No. 4.2e-99;
Matches 391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 106 CTTGTTTTCCCGGTTCTGTTTTCTCCCGAAGGCTTGTCAGGGGTAGGA 165
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QY 465 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 500
Db 360 AAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTT 394
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Job time : 997.903 secs



GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 84.1175 Seconds  
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Maximum Match 100%

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#### SUMMARIES

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| 3          | 492.6 | 98.5          | 10474  | 22 | AAF24685 Nucleotide sequenc |
| 4          | 492.6 | 98.5          | 10474  | 22 | AAF24686 Nucleotide sequenc |
| 5          | 492.6 | 98.5          | 10474  | 22 | AAF24707 Nucleotide sequenc |
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| 10 | 483.2 | 96.6 | 7086  | 22 | AAK52667 Human polynucleoti |
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| 45 | 92    | 18.4 | 11754 | 22 | AAK52667 Human ABC1 gene, p |

#### ALIGNMENTS

#### RESULT 1

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ID AAF24680 standard; DNA; 10442 BP.

AC AAF24680;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of a human ABC1 polypeptide.

KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 291..7076

FT /\*tag= a

FT /product= "ABC1 polypeptide"

PN WO200078972-A2.

PD 28-DEC-2000.

PE 16-JUN-2000; 2000WO-US16765.

PR 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-0166573.

XX

(CVTH-) CV THERAPEUTICS INC.

Lawn RM, Wade D, Garvin M;

WPI; 2001-137812/14.

Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis -

Disclosure; Page 122-128; 215pp; English.

The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilizes ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilization of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterized by abnormal HDL-cholesterol metabolism. The ABC1 gene is localized to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

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Best Local Similarity 100.0%; Pred. No. 1.1e-144;  
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QY 181 ACARAAGTGGAACAGTAATGACCAAGCGGCGTCTGCTGCTGCTGCTGCTGCTGCTG 240

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QY 241 TGCCTTCCAGGCTCCGAGCCACACGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTG 300

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QY 301 GGCCTCAGCTGAGTGTGCTGTGGAGAACCTTCATTTTCAGAGAGAGACAAATGTC 360

Db 301 GGCCTCAGCTGAGTGTGCTGTGGAGAACCTTCATTTTCAGAGAGAGACAAATGTC 360

QY 361 AGCTGTTACTGGAAGTGGCTGGCTCTATTTATCTTCTGATCTCTGCTGCTGCTG 420

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QY 421 TGAGTACCCACCTATGAACAAATGAATGCCATTTTCCAAATFAAGCCATGCCCTCTG 480

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AAF24702

ID AAF24702 standard; DNA: 10442 BP.

XX AAF24702;

DT 20-APR-2001 (first entry)

XX Nucleotide sequence of a human ABC1 polypeptide.

Human; adenosine triphosphate binding cassette protein 1; ABC1; apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9q22-9q31; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 291..7076

FT /tag= a /product= "ABC1 polypeptide"

XX WC200078971-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16591.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX (CVTH-) CV THERAPEUTICS INC.

XX (UNIW) UNIV WASHINGTON.

XX Lawn RM, Wade D, Oram JF, Garvin M;

XX WPI; 2001-137811/14.

XX P-PSDB; AAB31365.

Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis -

XX Claim 3; Page 117-123; 211pp; English.

The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilizes ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.

SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 500; DB 22; Length 10442;

Best Local Similarity 100.0%; Pred. No. 1.1e-144;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCGGACCCGAGCGGAGCGGACCCCTTCTCTCCGGGCTCGCGAGGCGGCGG 60

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RESULT 3  
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XX AAF24685;  
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XX  
DT 20-APR-2001 (first entry)  
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 323..7108  
FT CDS  
FT /\*tag= a  
FT /product= "defective ABC1 polypeptide"  
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PN WO200078972-A2.  
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XX 28-DEC-2000.  
XX 16-JUN-2000; 2000WO-US16765.  
XX  
XX 18-JUN-1999; 99US-0140264.  
PR 14-SEP-1999; 99US-0153872.  
PR 19-NOV-1999; 99US-0166573.  
XX  
XX (CVTH-) CV THERAPEUTICS INC.  
XX  
XX Lawn RM, Wade D, Garvin M;  
PI WPI; 2001-137812/14.  
XX  
XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
PT useful for the development of agents for the treatment of heart disease  
PT and other disorders associated with hypercholesterolemia and

atherosclerosis -  
PT  
XX  
PS Disclosure; Page 148-154; 215pp; English.  
XX  
CC The present sequence encodes a human adenosine triphosphate (ATP)  
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
CC ATP hydrolysis to transport a wide variety of substrates across the  
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;  
Query Match 98.5%; Score 492.6; DB 22; Length 10474;  
Best Local Similarity 99.2%; Pred. No. 2.3e-142;  
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GCGGGGACCGCAGAGCGGCGGACCTTCTCCCGGCTGCGGAGGCGAGGCGCGG 61  
Db 34 GGCACGAGCGCGAGAGCGGCGGACCTTCTCTCCGGGCTGCGGAGGCGAGGCGCGG 93  
QY 62 GAGCTCCGGGACCAACAGAGCGGTTCTCAGGGCGCTTTCCTCTGTTTTCCTCGG 121  
Db 94 GAGCTCCGGGACCAACAGAGCGGTTCTCAGGGCGCTTTCCTCTGTTTTCCTCGG 153  
QY 122 TTCTGTTTTCCTCCCTTCTCCGGAAGGCTGTCAGGGGTAGGAGAAAGACGCAACA 181  
Db 154 TTCTGTTTTCCTCCCTTCTCCGGAAGGCTGTCAGGGGTAGGAGAAAGACGCAACA 213  
QY 182 CAAAAGTGGAAACAGTAAATGACGAGCCACGGGCGTCCCTGCTGTGAGCTCTGCGCGT 241  
Db 214 CAAAAGTGGAAACAGTAAATGACGAGCCACGGGCGTCCCTGCTGTGAGCTCTGCGCGT 273  
QY 242 GCCTTCCAGGGTCCCGAGCCACAGCTGGGGCTGCTGGCTGAGGGAACATGGCTTTG 301  
Db 274 GCCTTCCAGGGTCCCGAGCCACAGCTGGGGCTGCTGGCTGAGGGAACATGGCTTTG 333  
QY 302 GCCTCAGCTGAGGTTGCTGCTGGAAGAACCTCACTTTCAGAAAGACAAACATGTCA 361  
Db 334 GCCTCAGCTGAGGTTGCTGCTGGAAGAACCTCACTTTCAGAAAGACAAACATGTCA 393  
QY 362 GCTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCTGATCCTGATCTCTGTTGCGCT 421  
Db 394 GCTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCTGATCCTGATCTCTGTTGCGCT 453  
QY 422 GAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAGCCATGCCCTCTGC 481  
Db 454 GAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAGCCATGCCCTCTGC 513  
QY 482 AGGAACACTTCTCTGGGTT 500  
Db 514 AGGAACACTTCTCTGGGTT 532

RESULT 4  
AAF24686  
ID AAF24686 standard; DNA; 10474 BP.  
XX AAF24686;  
XX  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX CDS 323..7108  
 XX FT /\*tag= a  
 XX FT /product= "defective ABC1 polypeptide"  
 XX PN WO200078972-A2.  
 XX PD 28-DEC-2000.  
 XX PF 16-JUN-2000; 2000WO-US16765.  
 XX PR 18-JUN-1999; 99US-0140264.  
 XX PR 14-SEP-1999; 99US-0153872.  
 XX PR 19-NOV-1999; 99US-0166573.  
 XX PA (CVTH-) CV THERAPEUTICS INC.  
 XX PI Lawn RM, Wade D, Garvin M;  
 XX WI: 2001-137812/14.  
 XX AD Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 PT useful for the development of agents for the treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX PS Disclosure; Page 170-176; 215pp; English.  
 XX CC The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
 CC ATP hydrolysis to transport a wide variety of substrates across the  
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
 CC Tangier disease, a genetic disorder characterised by abnormal  
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
 CC 9q22-q31. The ABC1 genes and proteins are useful for developing  
 CC pharmaceutical agents for the treatment of heart disease and other  
 CC disorders associated with hypercholesterolemia and atherosclerosis. The  
 CC genes are useful for developing screening assays to screen for compounds  
 CC that regulate the expression of genes associated with cholesterol  
 CC transport. The genes and proteins are also useful for are also useful  
 CC as diagnostic indicators of cardiovascular disease and other disorders  
 CC associated with hypercholesterolemia.  
 XX SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;  
 Query Match 98.5%; Score 492.6; DB 22; Length 10474;  
 Best Local Similarity 99.2%; Pred. No. 2.3e-142;  
 Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 GCGGGAGCCGCGAGCGGACCGACCTTCTCTCCGGGCTGCGGAGGCGGCGGG 61  
 DB 34 GGCAGAGCGCGGAGCGGAGCGGACCGCTTCTCTCCGGGCTGCGGAGGCGGCGGG 93  
 QY 62 GAGCTCCGCGCCACCAACAGAGCGGTTCTCAGGCGCTTGTCTCTTTTTCGCCGG 121  
 DB 94 GAGCTCCGCGCCACCAACAGAGCGGTTCTCAGGCGCTTGTCTCTTTTTCGCCGG 153  
 QY 122 TTCTGTTTCTCCCTTCTCCGAGGCTTGTCAAGGCGGTAGGAGAAAGACGCAACA 181  
 DB 154 TTCTGTTTCTCCCTTCTCCGAGGCTTGTCAAGGCGGTAGGAGAAAGACGCAACA 213  
 QY 182 CAAAAGTGGAAACAGTTAATCACCAGGCGGCGCTCCCTGCTGTGAGCTCGGCCCT 241

DB 214 CAAAAGTGGAAACAGTTAATGACCCAGCGGCGTCCCTGCTGTGAGCTCTGGCGCT 273  
 QY 242 GCCTTCCAGGCGTCCGAGCCACACGCTGGCGTGTCTGGCTGAGGGAACATGGCTTGTG 301  
 DB 274 GCCTTCCAGGCGTCCGAGCCACACGCTGGCGTGTCTGGCTGAGGGAACATGGCTTGTG 333  
 QY 302 GCCTCAGCTGAGGTTGCTGTGTGGGAAGAACCTCCTACCTTCAGAGAAGACAAACATGTCA 361  
 DB 334 GCCTCAGCTGAGGTTGCTGTGTGGGAAGAACCTCCTACCTTCAGAGAAGACAAACATGTCA 393  
 QY 362 GCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCTGATCTCTGATCTCTGCGGT 421  
 DB 394 GCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCTGATCTCTGATCTCTGCGGT 453  
 QY 422 GAGTACCCACCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 481  
 DB 454 GAGTACCCACCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTGC 513  
 QY 482 AGGAACACTTCTTGGGTT 500  
 DB 514 AGGAACACTTCTTGGGTT 532  
 RESULT 5  
 AAF24707  
 ID AAF24707 standard; DNA; 10474 BP.  
 XX AC AAF24707;  
 XX DT 20-APR-2001 (first entry)  
 XX DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
 XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX CDS 323..7108  
 XX FT /\*tag= a  
 XX FT /product= "defective ABC1 polypeptide"  
 XX PN WO200078971-A2.  
 XX PD 28-DEC-2000.  
 XX PF 16-JUN-2000; 2000WO-US16591.  
 XX PR 18-JUN-1999; 99US-0140264.  
 XX PR 14-SEP-1999; 99US-0153872.  
 XX PR 19-NOV-1999; 99US-0166573.  
 XX PA (CVTH-) CV THERAPEUTICS INC.  
 XX PI (UNIW) UNIV WASHINGTON.  
 XX PI Lawn RM, Wade D, Oram JF, Garvin M;  
 XX WI: 2001-137811/14.  
 XX DR P-PSDB; AAB31366.  
 XX AD Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
 PT polynucleotides and polypeptides, useful for treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX PS Claim 27; Page 144-150; 211pp; English.  
 XX CC The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises

CC ATP hydrolysis to transport a wide variety of substrates across the  
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 98.5%; Score 492.6; DB 22; Length 10474;  
Best Local Similarity 99.2%; Pred. No. 2.3e-142;  
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GCCGGGACCCGAGACGCGGACCGGACCGGCTTCTCCCGGGCTGCGGACGAGCGGCGGG 61  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 34 GGCACGAGCGCGAGACGCGGACCGGACCGGCTTCTCCCGGGCTGCGGACGAGCGGCGGG 93  
QY 62 GAGCTCCCGGACCAACAGAGCGGCTTCTCAGGGGCTTTGCTCTCTTTTTCCTCCCGG 121  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 94 GAGCTCCCGGACCAACAGAGCGGCTTCTCAGGGGCTTTGCTCTCTTTTTCCTCCCGG 153  
QY 122 TTCTGTTTCTCCCGCTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAACA 181  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 154 TTCTGTTTCTCCCGCTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAACA 213  
QY 182 CAAAGTGGAAACAGTTAATGACACGCGGCGTCCCTGCTGAGCTTGGCCGCT 241  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 214 CAAAGTGGAAACAGTTAATGACACGCGGCGTCCCTGCTGAGCTTGGCCGCT 273  
QY 242 GCCTTCCAGGGCTCCCGGACCAACAGCGTGGGCTGCTGGCTGAGGGAACATGGCTTGTG 301  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 274 GCCTTCCAGGGCTCCCGGACCAACAGCGTGGGCTGCTGGCTGAGGGAACATGGCTTGTG 333  
QY 302 GCCTCAGCTAGGTTGCTGCTGAGGAAACCTCACTTTCAGAGAAACAAACATGCA 361  
DB 334 GCCTCAGCTAGGTTGCTGCTGAGGAAACCTCACTTTCAGAGAAACAAACATGCA 393  
QY 362 GCTGTTACTGGAAGTGGGCTGGCCCTATTATCTTCTGATCCCTGATCTCTGTTCCGCT 421  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 394 GCTGTTACTGGAAGTGGGCTGGCCCTATTATCTTCTGATCCCTGATCTCTGTTCCGCT 453  
QY 422 GAGTATCCACCCCTATGAAACACATGATGCGCATTTTCCAAATAAGCCATGCCCTCTGC 481  
DB 454 GAGTATCCACCCCTATGAAACACATGATGCGCATTTTCCAAATAAGCCATGCCCTCTGC 513  
QY 482 AGGAACACTTCTCTGGGT 500  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 514 AGGAACACTTCTCTGGGT 532

RESULT 6  
AAF24708  
ID AAF24708 standard; DNA; 10474 BP.  
XX AAF24708;  
AC AAF24708;  
XX 20-APR-2001 (first entry)  
DT  
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
XX Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.  
XX Homo sapiens.  
OS

XX Key Location/Qualifiers  
FH CDS 323..7108  
FT /\*tag= a  
FT /product= "defective ABC1 polypeptide"  
XX  
PN WC200078971-A2.  
XX  
PD 28-DEC-2000.  
XX  
PF 16-JUN-2000; 2000WO-US16591.  
XX  
PR 18-JUN-1999; 99US-0140264.  
PR 14-SEP-1999; 99US-0153872.  
PR 19-NOV-1999; 99US-0166573.  
XX  
XX (CVTH-) CV THERAPEUTICS INC.  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Lawn RM, Wade D, Oram JF, Garvin M;  
PI  
XX WPI; 2001-137811/14.  
DR P-PSDB; AAB31367.  
XX  
PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
PT polynucleotides and polypeptides, useful for treatment of heart disease  
PT and other disorders associated with hypercholesterolemia and  
PT atherosclerosis.  
PS Claim 30; Page 165-172; 211pp; English.  
XX  
CC The present sequence encodes a human adenosine triphosphate (ATP)  
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
CC ATP hydrolysis to transport a wide variety of substrates across the  
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;

Query Match 98.5%; Score 492.6; DB 22; Length 10474;  
Best Local Similarity 99.2%; Pred. No. 2.3e-142;  
Matches 495; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 GCCGGGACCCGAGACGCGGACCGGACCGGCTTCTCCCGGGCTGCGGACGAGCGGCGGG 61  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 34 GGCACGAGCGCGAGACGCGGACCGGACCGGCTTCTCCCGGGCTGCGGACGAGCGGCGGG 93  
QY 62 GAGCTCCCGGACCAACAGAGCGGCTTCTCAGGGGCTTTGCTCTCTTTTTCCTCCCGG 121  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 94 GAGCTCCCGGACCAACAGAGCGGCTTCTCAGGGGCTTTGCTCTCTTTTTCCTCCCGG 153  
QY 122 TTCTGTTTCTCCCGCTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAACA 181  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 154 TTCTGTTTCTCCCGCTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAACA 213  
QY 182 CAAAGTGGAAACAGTTAATGACACGCGGCGTCCCTGCTGAGCTTGGCCGCT 241  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 214 CAAAGTGGAAACAGTTAATGACACGCGGCGTCCCTGCTGAGCTTGGCCGCT 273  
QY 242 GCCTTCCAGGGCTCCCGGACCAACAGCGTGGGCTGCTGGCTGAGGGAACATGGCTTGTG 301  
DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 274 GCCTTCCAGGGCTCCCGGACCAACAGCGTGGGCTGCTGGCTGAGGGAACATGGCTTGTG 333

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QY 302 GCTCAGCTGAGTTGCTGCTGTGAAGAACCTCATTTCAGAGAACAGACAAATGTC 361
DB 334 GCTCAGCTGAGTTGCTGCTGTGAAGAACCTCATTTCAGAGAACAGACAAATGTC 393
QY 362 GCTGTTACTGGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
DB 394 GCTGTTACTGGAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 453
QY 422 GAGCTACCCACCTATGAACACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
DB 454 GAGCTACCCACCTATGAACACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 513
QY 482 AGGAACACTTCCTGGGTT 500
DB 514 AGGAACACTTCCTGGGTT 532

RESULT 7
AAD21326
ID AAD21326 standard; DNA; 7260 BP.
AC AAD21326;
XX
XX
DT 28-JAN-2002 (first entry)
DE Human ATP binding cassette transporter 1 (ABCI) gene.
KW Human: ATP binding cassette transporter 1; ABC1; coronary heart disease;
KW dermatological; atherosclerosis; cardiovascular; inflammatory disease;
KW psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
KW immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 321..7106
FT /*tag= a
FT /product= "Human ABC1 protein"
XX
XX
PN EP1136552-A1.
XX
XX
PD 26-SEP-2001.
XX
XX
PF 20-MAR-2000; 2000EP-0105820.
XX
XX
PR 20-MAR-2000; 2000EP-0105820.
XX
XX
PA (FARB ) BAYER AG.
XX
PI Schmitz G, Bodzioch M;
XX
XX
DR WPI; 2001-640388/74.
DR P-PSDB; AAE13022.
XX
XX
New adenosine triphosphate binding cassette transporter-1 gene
XX polymorphisms, useful for diagnosing and treating lipid disorders,
XX cardiovascular diseases and inflammatory diseases
XX
XX
Example 1; Fig 1; 48pp; English.
XX
XX
The invention relates to four common polymorphisms in the gene encoding
XX ATP-binding cassette transporter-1 (ABCI). ABC1 is associated with
XX decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
XX ABC1 directly affects cellular lipid homeostasis, which is a key factor
XX in the atherogenetic processes. The ABC1 polymorphisms are useful for
XX diagnosing and treating lipid disorders, cardiovascular diseases
XX (coronary heart disease, atherosclerosis) and inflammatory diseases
XX (psoriasis, lupus erythematosus). The identification of ABC1 as a
XX transporter for interleukin-beta (IL-beta) identifies this gene as
XX a candidate for treatment of inflammatory diseases including rheumatoid
XX arthritis and septic shock. The present sequence is human ABC1 gene.

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SO Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
Query Match 97.3%; Score 486.4; DB 22; Length 7260;
Best Local Similarity 99.6%; Pred. No. 1.5e-140;
Matches 498; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GGCCGGACCCGAGAGCCGAGCCGAGCCCTCTCTCCCGGGCTGCGGAGGCGAGGCGG 60
DB 32 GGCCGGAGCCGAGAGCCGAGCCGAGCCCTCTCTCCCGGGCTGCGGAGGCGAGGCGG 91
QY 61 GGAGCTCCGCGCCACCAACAGAGCCGCTTCTCAGGGGCTTTGCTCTCTTTTTCCTCG 120
DB 92 GGAGCTCCGCGCCACCAACAGAGCCGCTTCTCAGGGGCTTTGCTCTCTTTTTCCTCG 151
QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAAC 180
DB 152 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAAC 211
QY 181 ACAAAAGTGAAACAGTTAATGACGAGCCAGCCGCGCTCCCTGCTGAGCTTGCGCCG 240
DB 212 ACAAAAGTGAAACAGTTAATGACGAGCCAC-GGGCTCCCTGCTGAGCTTGCGCCG 270
QY 241 TGCCTCCAGGGCTCCGAGCCACAGCTGGGCTGCTGGCTGAGGGAACATGGCTTGT 300
DB 271 TGCCTCCAGGGCTCCGAGCCACAGCTGGGCTGCTGGCTGAGGGAACATGGCTTGT 330
QY 301 GGCTCAGCTGAGTTGCTGCTGTGAAGAACCTCATTTCAGAGAACAGACAAATGTC 360
DB 331 GGCTCAGCTGAGTTGCTGCTGTGAAGAACCTCATTTCAGAGAACAGACAAATGTC 390
QY 361 AGCTGTTACTGGAAGTGGCTGCGCTCTATTATCTCTGATCTCTGTTTCGCG 420
DB 391 AGCTGTTACTGGAAGTGGCTGCGCTCTATTATCTCTGATCTCTGTTTCGCG 450
QY 421 TGAGCTACCCACCTATGAACACATGATGATGATGATGATGATGATGATGATGATG 480
DB 451 TGAGCTACCCACCTATGAACACATGATGATGATGATGATGATGATGATGATGATG 510
QY 481 CAGGAACACTTCCTGGGTT 500
DB 511 CAGGAACACTTCCTGGGTT 530

RESULT 8
AAI70315
ID AAI70315 standard; cDNA; 7260 BP.
XX
XX
AC AAI70315;
XX
XX
DT 07-JAN-2002 (first entry)
DE Human ATP binding cassette transporter 1 (ABCI) cDNA.
XX
XX
KW ATP binding cassette transporter 1; ABC1; human; lipid disorder;
KW cholesterol; cardiovascular disease; inflammatory disease;
KW antinflammatory; antilipemic; antipsoriatic; dermatological;
KW Tangier disease; coronary heart disease; diagnosis; gene therapy;
KW polymorphism; ss.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 321..7106
FT /*tag= a
FT CDS 501..7106
FT /*tag= b
FT variation /note= "alternative open reading frame of AAI70314"
FT replace(976,A)
FT variation /*tag= c
FT variation replace(1516,C)
FT variation /*tag= d
FT variation replace(2969,G)
FT /*tag= e

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FT variation replace(3836,C)
FT /tag= f
XX EP1136554-AL.
XX
XX PD 26-SEP-2001.
XX PF 24-MAR-2000; 2000EP-0106401.
XX PR 24-MAR-2000; 2000EP-0106401.
XX PA (FARB ) BAYER AG.
XX Schmitz G, Bodzioch M;
XX PI WPI; 2001-640389/74.
XX DR P-PSDB; AAM50228.
XX
XX New adenosine triphosphate binding cassette transporter gene
PT polymorphisms, useful for diagnosing and treating lipid disorders,
PT cardiovascular diseases and inflammatory diseases
XX Disclosure; Page 26-28; 4lpp; English.
XX
CC The present sequence is that of cDNA encoding the human adenosine
CC triphosphate (ATP) binding cassette transporter 1 (ABCI1) protein
CC (see AAM50227). That sequence includes an extended open reading
CC frame (ORF) to that provided by the sequence in AA170314, using
CC an alternative ATG codon as initiation codon and thereby adding an
CC extra 40 N-terminal amino acids to the encoded ABCI1 protein (see
CC AAM50228). The invention provides 4 common polymorphisms in the
CC ABCI1 gene. These were identified by sequencing the ABCI1 gene in
CC different Tangier kindreds. In the variant genes (numbering as in
CC AA170314), G is changed to A at position 596, T is changed to C at
CC position 1136, A is changed to G at position 2589 or G is changed
CC to C at position 3456, or any combination of these. All of these
CC polymorphisms alter the amino acid sequence of ABCI1 and therefore
CC may affect its function. The 2 most common polymorphisms (GS96A)
CC and A2589G are both associated with a decreased in vitro ApoA-I
CC mediated efflux of cholesterol from mononuclear phagocytes, a
CC feature typical of Tangier disease. 3 Of the variants (GS96A,
CC A2589G and G3456C) are significantly increased in a population of
CC men having low high density lipoprotein-cholesterol levels and
CC established coronary heart disease (CHD) relative to CHD-free
CC control subjects. The use of the provided ABCI1 polymorphisms for
CC the diagnosis and treatment of lipid disorders, cardiovascular
CC diseases, and inflammatory diseases (e.g. psoriasis, lupus
CC erythematoses) is claimed. Modulation of ABCI1 transcripts or
CC proteins by antisense or ribozyme technology or RNA decoys is also
CC claimed.
XX
SQ Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match          97.3%; Score 486.4; DB 22; Length 7260;
Best Local Similarity 99.6%; Pred. No. 1.6e-140;
Matches 498; Conservative 0; Mismatches 1; Indels 1; Gaps

QY      1  GGCGGGACCGAGAGCCGAGCCGCCGACCCTTCTCTCCCGGGTGCGGAGGCAGGCGCG 60
       |||
Db       32  GGCGGGACCGGAGAGCCGAGCCGCCGACCCTTCTCTCCCGGGTGCGGAGGCAGGCGCG 91
       |||

QY      61  GGAGCTCGGCGACCAACAGAGCGGTTCTTCAGGGCGCTTTGTCTCTCTGTTTTTCCCCG 120
       |||

Db       92  GGAGCTCGGCGACCAACAGAGCGGTTCTTCAGGGCGCTTTGTCTCTCTGTTTTTCCCCG 151
       |||

QY     121  GTTCTGTTTTTCTCCCCTTCTCCGGAGGCTTGTCAGGGGTAGGAAGAAGACGCNAAC 180
       |||

Db     152  GTTCTGTTTTTCTCCCCTTCTCCGGAGGCTTGTCAGGGGTAGGAAGAAGACGCNAAC 211
       |||

QY     181  ACAAAAGTGAACAACAGTTTAATGACCAGCACCGGGCGTCTCTCTCTGTAGCTCTGGCCGC 240
       |||

Db     212  ACAAAAGTGAACAACAGTTTAATGACCAGCAC -GGGGTCCCTGCTGTAGCTCTGGCCGC 270

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|          |   |   |     |
|----------|---|---|-----|
| Qy       | 241   | TGCTTCCAGGGCTCCGAGACCCACACGCTGGCGCTGGCTGAGGAAACATGGCTTGT      | 300 |
|          |   |   |     |
| Db       | 271   | TGCTTCCAGGGCTCCGAGACCCACACGCTGGGGTGCCTGGCTGAGGAAACATGGCTTGT   | 330 |
|          |   |   |     |
| Qy       | 301   | GGCTTCAGCTGAGGTTGCTGTGTGGAACAACCTCACATTTTCAGAAGAAGACAAACATGTC | 360 |
|          |   |   |     |
| Db       | 331   | GGCTTCAGCTGAGGTTGCTGTGTGGAACAACCTCACATTTTCAGAAGAAGACAAACATGTC | 390 |
|          |   |   |     |
| Qy       | 361   | AGCTGTTACTGGAAGTGGCGCTGGCTCTATTATCTTCTGATCTGATCTCTTTCGGC      | 420 |
|          |   |   |     |
| Db       | 391   | AGCTGTTACTGGAAGTGGCGCTGGCTCTATTATCTTCTGATCTGATCTCTTTCGGC      | 450 |
|          |   |   |     |
| Qy       | 421   | TGAGCTACCCACCCCTATGAACACATGAATGCATTTTCCAAATAAAGCCATGCCCTCTG   | 480 |
|          |   |   |     |
| Db       | 451   | TGAGCTACCCACCCCTATGAACACATGAATGCATTTTCCAAATAAAGCCATGCCCTCTG   | 510 |
|          |   |   |     |
| Qy       | 481   | CAGGAACACTTCCTTGGGTT  | 500 |
|          |   |   |     |
| Db       | 511   | CAGGAACACTTCCTTGGGTT  | 530 |
|          |   |   |     |
| RESULT 9 |   |   |     |
| ABA09200 |   |   |     |
| ID       | ABA09200 standard; cdNA; 7086 BP.   |   |     |
| XX       | AC  | ABA09200;   |     |
| XX       | XX  |   |     |
| DT       | 11-JAN-2002 (first entry)   |   |     |
| XX       |   |   |     |
| DE       | Human ABCA1 homologue-encoding cdNA, SEQ ID NO:976.                       |   |     |
| XX       |   |   |     |
| Kw       | Human; cytokine; cell proliferation; cell differentiation; growth factor; |   |     |
| Kw       | haematopoiesis regulation; tissue growth; immunomodulator; activin;       |   |     |
| Kw       | inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;             |   |     |
| Kw       | proliferation; metastasis; cancer; tumour; haematopoietic disorder;       |   |     |
| Kw       | myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;         |   |     |
| Kw       | chronic inflammatory condition; proliferative retinopathy;                |   |     |
| Kw       | atherosclerosis; coronary heart disease; arterial ischaemia;              |   |     |
| Kw       | bone disorder; osteoporosis; vascular growth disorder;                    |   |     |
| Kw       | tissue regeneration; wound healing; infection; immune disorder;           |   |     |
| Kw       | cell culture; drug screening; gene therapy; antiinflammatory;             |   |     |
| Kw       | antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;          |   |     |
| Kw       | cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;    |   |     |
| Kw       | antifungal; vulvar; antitumor; ss.  |   |     |

## RESULT 9

ABA09200  
ID ABA09200 standard; cDNA; 7086 BP.

AA ABA09200:

XX  
60897

DT 11-JAN-2002 (first entry)

XX  
DE  
Human ABCA1 homologue-encoding cDNA, SEQ ID NO:976.

Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnervary; antitumor; ss.

OS Homo sapiens.

XX PN WO200157188-A2.

XX  
PD 09-AUG-2001.

05-FEB-2001: 2001WO-US03800

03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.  
XX

PA (HYSE-) HYSEQ INC.

XX  
PI  
Tang YT, Liu C, Drmanac RT;

XX  
DR WPI; 2001-457740/49.

DR P-PSDB; ABB11956.

xx Human proteins and DNA encoding sequences useful for preventing,  
PT treating or ameliorating a medical condition in a mammalian subject  
PT e.g. arthritis and cancer -

PS Claim 1; page 833-835; 1963pp; English.  
XX

xx  
cc Sequences ABB10981-ABB1230 represent 1350 novel human polypeptides, and  
cc sequences ABA08223-ABA09574 represent nucleic acids encoding them. The  
cc invention also relates to vectors and recombinant host cells comprising a  
cc nucleotide of the invention, methods of producing the novel polypeptides  
cc

antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; activin- or inhibin-related activities; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

Query Match 96.6%; Score 483.2; DB 22; Length 7086;  
Best Local Similarity 99.2%; Pred. No. 1.6e-139;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCGCGGACCGCAGCGGACCGACCGCTCTCTCCGGGCTCGCGAGGCGGCGG 60  
DB 15 GCGCGGACCGCAGCGGACCGACCGCTCTCTCCGGGCTCGCGAGGCGGCGG 74  
QY 61 GGAGCTCGCGCACCACAGACGCGGTTCTCAGGCGGCTTGTCTCTCTCTCTCTCCCG 120  
DB 75 GGAGCTCGCGCACCACAGACGCGGTTCTCAGGCGGCTTGTCTCTCTCTCTCTCCCG 134  
QY 121 GTTCTGTTTCT 180  
DB 135 GTTCTGTTTCT 194  
QY 181 ACAAAAGTGGAAACAGTAAATACACAGCGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
DB 195 ACAAAAGTGGAAACAGTAAATACACAGCGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCT 253  
QY 241 TGCCTTCAGGCGTCCGAGCCACGCTGGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300  
DB 254 TGCCTTCAGGCGTCCGAGCCACGCTGGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313  
QY 301 GGCCTCAGCTGAGTGTCTGT 360  
DB 314 GGCCTCAGCTGAGTGTCTGT 373  
QY 361 AGCTGTACTGGAAGTGGCGCTCTATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
DB 374 AGCTGTACTGGAAGTGGCGCTCTATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 433  
QY 421 TGAGTACCCACCTTACACATGAATGCGATTTTCCAAATAGCCATGCCCTCTG 480  
DB 434 TGAGTACCCACCTTACACATGAATGCGATTTTCCAAATAGCCATGCCCTCTG 493  
QY 481 CAGGAACACTTCTCTGGGTT 500

Db 494 CAGGAACACTTCTCTGGGTT 513

RESULT 10

AAK52667  
ID AAK52667 standard; cDNA; 7086 BP.

XX AAK52667;

DT 06-NOV-2001 (first entry)

XX Human polynucleotide SEQ ID NO 2196.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens.

XX WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX 20-JUN-2000; 2000US-0598075.

XX 19-JUL-2000; 2000US-0620325.

XX 01-SEP-2000; 2000US-0654936.

XX 15-SEP-2000; 2000US-0663561.

XX 20-OCT-2000; 2000US-0693325.

XX 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejman T, Goodrich R;

XX WPI; 2001-476283/51.

XX P-PSDB; AAM79534.

XX Nucleic acids encoding polypeptides with cytokine-like activities,  
XX useful in diagnosis and gene therapy -

XX Claim 1; Page 4558-4560; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.

XX Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;

Query Match 96.6%; Score 483.2; DB 22; Length 7086;  
Best Local Similarity 99.2%; Pred. No. 1.6e-139;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GCGCGGACCGCAGCGGACCGACCGCTCTCTCCGGGCTCGCGAGGCGGCGG 60  
|||||



XX Human ABC1 DNA sequence #2.  
 DE  
 XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
 KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
 KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 298..7078  
 FT /\*tag= a  
 FT /product= "Human ABC1 protein"  
 XX  
 PN WO200130848-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000WO-EP10886.  
 XX  
 PR 26-OCT-1999; 99EP-0402668.  
 PR 01-MAR-2000; 2000US-0186260.  
 XX  
 PA (AVET ) AVENTIS PHARMA SA.  
 XX  
 PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;  
 PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
 PI Dean M;  
 XX  
 DR WPI; 2001-316327/33.  
 DR P-PSDB; AAU02176.  
 XX  
 PT New human ABC1 nucleic acids and polypeptides for treating  
 PT atherosclerosis, malaria and diabetes  
 XX  
 PS Claim 1; Page 209-213; 368pp; English.  
 XX  
 CC The sequence represents the coding sequence #2 of human ABC1. The  
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,  
 CC and polypeptides and vectors are useful for the prevention of  
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse  
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is  
 CC useful for screening for an active ingredient for the prevention or  
 CC treatment of a disease resulting from dysfunction in the reverse  
 CC transport of cholesterol. The nucleic acids and polypeptides are also  
 CC useful for treating and preventing cardiovascular and neurological  
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-  
 CC cholesterol (LCAT) deficiency, malaria and diabetes.  
 XX  
 SQ Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;

Query Match 96.6%; Score 483.2; DB 22; Length 9854;  
 Best Local Similarity 99.2%; Pred. No. 1.9e-139;  
 Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
 1 GCGCGGACCCGACAGCCGAGCGACCCCTCTCTCCGGCGCTCGCGCAGGGCAGGCGG 60  
 9 GCGCGGACCCGAGCGGAGCGACCCCTCTCTCCGGCGCTCGCGCAGGGCAGGCGG 68  
 61 GGAGCTCGCGCACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTGTTTTCCTCCG 120  
 69 GGAGCTCGCGCACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTGTTTTCCTCCG 128  
 121 GTTCTGTTTTCCTCCCTTCCTCCGAGAGCTTGCTCAAGGGGTAGAGAAAGAGCGCAAC 180  
 129 GTTCTGTTTTCCTCCCTTCCTCCGAGAGCTTGCTCAAGGGGTAGAGAAAGAGCGCAAC 188  
 181 ACAAAGTGGAAAACAGTTAATGACCAAGCCAGCGGCTTCCTGCTGTGAGCTCTGGCCG 240  
 189 ACAAAGTGGAAAACAGTTAATGACCAAGCCAGCGGCTTCCTGCTGTGAGCTCTGGCCG 247  
 241 TGCCTTCAGGGCTTCGCGAGCCACACGCTGGGCTGTGCTGAGGGAACATGGCTTGT 300

Db 248 TGCTTCCAGGGCTCCGAGCCACACGCTGGGGTGCTGGCTGAGGAAACATGGCTTGT 307  
 QY 301 GGCCTCAGCTCAGGTTGCTGTGGAAGAACCTCAGTTTCAGAAGAAGACAACATGTC 360  
 Db 308 GGCCTCAGCTCAGGTTGCTGTGGAAGAACCTCAGTTTCAGAAGAAGACAACATGTC 367  
 QY 361 AGCTGTACTGGAAGTGGCCTCTATTATCTTCCTGATCCTGATCTCTGTTCGGC 420  
 Db 368 AGCTGTGCTGGAAGTGGCCTCTATTATCTTCCTGATCCTGATCTCTGTTCGGC 427  
 QY 421 TGAGTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCG 480  
 Db 428 TGAGTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCG 487  
 QY 481 CAGGACACTTCCTTGGGTT 500  
 Db 488 CAGGACACTTCCTTGGGTT 507  
 XX  
 RESULT 13  
 AAH07432  
 ID AAH07432 standard; cDNA; 736 BP.  
 XX  
 AC AAH07432;  
 XX  
 DT 26-JUN-2001 (first entry)  
 XX  
 DE Human cDNA clone (5'-primer) SEQ ID NO:4267.  
 XX  
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1074617-A2.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 28-JUL-2000; 2000EP-0116126.  
 XX  
 PR 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 WIPI; 2001-318749/34.  
 DR  
 XX  
 PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX  
 PS Claim 1; SEQ ID 4267; 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,

|           |  |
|-----------|--|
| CC        | particularly full-length cDNAs. The primers are also useful for the        |
| CC        | detection and/or diagnosis of the abnormality of the proteins encoded by   |
| CC        | the full-length cDNAs. The primers allow obtaining of the full-length      |
| CC        | cDNAs easily without any specialised methods. AAH03166 to AAH13628 and     |
| CC        | AAH13633 to AAH18742 represent human cDNA sequences; AAB92445 to           |
| CC        | AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632    |
| CC        | represent oligonucleotides, all of which are used in the exemplification   |
| CC        | of the present invention.  |
| XX        |  |
| XX        | Sequence 736 BP; 163 A; 199 C; 199 G; 170 T; 5 other;                      |
| SQ        |  |
|           | Query Match 96.3%; Score 481.6; DB 22; Length 736;                         |
|           | Best Local Similarity 99.0%; Pred. No. 1.7e-139;                           |
|           | Matches 495; Conservative 0; Mismatches 4; Indels 1; Gaps                  |
| QY        | 1 GGCGGGACCCGAGACGCCGAGCCGACCCTTCTCTCCGGGTGCGGCAGGCGGCGG 50                |
| DB        | 25 GGCGGGACCCGAGACGCCGAGCCGACCCTTCTCTCCGGGTGCGGCAGGCGGCGG 84               |
| QY        | 61 GGAGCTCCGGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTGCTCTCTGTTTTTCOCGG 120         |
| DB        | 85 GGAGCTCCGGCGCACCAACAGAGCCGGTTCTCAGGGCGCTTGCTCTCTGTTTTTCOCGG 144         |
| QY        | 121 GTTCTGTTTTTCCCCTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAAC 180           |
| DB        | 145 GTTCTGTTTTTCCCCTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGACGCAAC 204           |
| QY        | 181 ACAAAAGTGAACAACAGTTTAATGACCAGCCACCGGCGTCCCTGCTGAGCTCTGCGCGC 240        |
| DB        | 205 ACAAAAGTGAACAACAGTTTAATGACCAGCCAC -GGCGTCCCTGCTGTGAGCTCTGCGCGC 263     |
| QY        | 241 TGCTTCCAGGGTCCCGAGCCACAGCTGGCGTGCTGGCTGAGGGAACATGGCTTGT 300            |
| DB        | 264 TGCTTCCAGGGTCCCGAGCCACAGCTGGCGTGCTGGCTGAGGGAACATGGCTTGT 323            |
| QY        | 301 GGCTCAGCTAGATTGCTGCTGTGGAGAACCCTACCTTTCAGAGAAGAACACATGTC 360           |
| DB        | 324 GGCCCCAGCTGAGGTTTGCTGCTGTGGAGAACCCTCACTTTCAGAGAAGAACACATGTC 383        |
| QY        | 361 AGCTGTTACTGGAAAGTGGCTGGCCTCATTTATCTTCCTGATCCTCATCTCTGTTCGGC 420        |
| DB        | 384 AGCTGCTGCTGGAGTGGCTGGCCTCATTTATCTTCCTGATCCTGATCTCTGTTCGGC 443          |
| QY        | 421 TGAGCTACCCACCCTATGACACACATGAATGCCATTTTCCAATAAAGCCATGCCCTCTG 480        |
| DB        | 444 TGAGCTACCCACCCTATGACACACATGAATGCCATTTTCCAATAAAGCCATGCCCTCTG 503        |
| QY        | 481 CAGGAACACTTCCCTGGGTT 500   |
| DB        | 504 CAGGAACACTTCCCTGGGTT 523   |
| RESULT 14 |  |
| AAH18606  |  |
| ID        | AAH18606 standard; cDNA; 1556 BP.  |
| XX        |  |
| AC        | AAH18606;  |
| XX        |  |
| DT        | 26-JUN-2001 (first entry)  |
| XX        |  |
| DE        | Human cDNA sequence SEQ ID NO:18808.                                       |
| XX        |  |
| KW        | Human; primer; detection; diagnosis; antisense therapy; gene therapy; iss; |
| OS        | Homo sapiens.  |
| PN        | EPI074617-A2.  |
| XX        |  |
| PD        | 07-FEB-2001.   |
| XX        |  |
| XX        | 28-JUL-2000; 2000EP-0116136.   |
| PR        | 29-JUL-1999; 99JP-0248036.   |

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Db 384 AGCTGCTGTGAAGTGGCTGGCTCTATTATCTTCTGATCTGATCTGTGTGGC 443
QY 421 TGAGCTACCCACCCCTATGAAACACATGAATGCCATTTCCAAATAAAGCCATGCCCTCTG 480
Db 444 TGAGCTACCCACCCCTATGAAACACATGAATGCCATTTCCAAATAAAGCCATGCCCTCTG 503
QY 481 CAGGAACACTTCTCTGGGTT 500
Db 504 CAGGAACACTTCTCTGGGTT 523

RESULT 15
AAS04035
ID AAS04035 standard; cDNA; 446 BP.
AC AAS04035;
XX
XX 12-SEP-2001 (first entry)
XX Partial human ABC1 cDNA sequence.
XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
XX cardiovascular; neurological; Tangier disease; LCAT deficiency;
XX lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 185..438
XX /*tag= a
XX /product= "Human ABC1 protein, amino acids 1 to 60"
XX
XX PN WO200130848-A2.
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-EPI0886.
XX
XX PR 26-OCT-1999; 99EP-0402668.
XX PR 01-MAR-2000; 2000US-0186260.
XX
XX (AVET ) AVENTIS PHARMA SA.
XX
XX PI Deneffe P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
XX PI Lemcine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
XX PI Dean M;
XX
XX WPI: 2001-316327/33.
XX P-PSDB: RAU02176.
XX
XX New human ABC1 nucleic acids and polypeptides for treating
XX atherosclerosis, malaria and diabetes -
XX
XX Example 2; Page 167; 368pp; English.
XX
XX The sequence represents the partial coding sequence of human ABC1,
XX which encodes amino acids 1-60 of the human ABC1 protein. The nucleic
XX acid sequence, primers and probes derived from the ABC1 sequence, and
XX polypeptides and vectors are useful for the prevention of
XX atherosclerosis, in a subject affected by a dysfunction in the reverse
XX transport of cholesterol. The polypeptide encoded by the ABC1 gene is
XX useful for screening for an active ingredient for the prevention or
XX treatment of a disease resulting from dysfunction in the reverse
XX transport of cholesterol. The nucleic acids and polypeptides are also
XX useful for treating and preventing cardiovascular and neurological
XX pathologies, and other diseases e.g. Tangier disease, lecithin-
XX cholesterol (LCAT) deficiency, malaria and diabetes.
XX
XX SQ Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;

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Query Match 75.6%; Score 378.2; DB 22; Length 446;  
 Best Local Similarity 99.0%; Pred. No. 2e-107;

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Matches 391; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 106 CTTGTTTTTCCCGGTTCTGTCTTCTCCCTCTCCGGAAGCTTGTCAAGGGGTAGGA 165
Db 1 CTTGTTTTTCCCGGTTCTGTCTTCTCCCTCTCCGGAAGCTTGTCAAGGGGTAGGA 60
QY 166 GAAAGAGACGCAAAACACAAAAGTGGAAAACAGTTAATGACCCAGCGTCCCTGCT 225
Db 61 GAAAGAGACGCAAAACACAAAAGTGGAAAACAGTTAATGACCCAGCGTCCCTGCT 119
QY 226 GTGAGCTCTGGCGCTGCCCTTCCAGGCTCCCGAGCCACACGCTGGCGTGGCTGAG 285
Db 120 GTGAGCTCTGGCGCTGCCCTTCCAGGCTCCCGAGCCACACGCTGGCGTGGCTGAG 179
QY 286 GGAACATGGCTTGTGGCTCAGCTGAGTGTGCTGTGGAAGAACCTCAGTTTCAGAA 345
Db 180 GGAACATGGCTTGTGGCTCAGCTGAGTGTGCTGTGGAAGAACCTCAGTTTCAGAA 239
QY 346 GAGACAAACATGTCAGCTGTTACTGGAAGTGGCTGCTATTATCTTCTCTGATCC 405
Db 240 GAGACAAACATGTCAGCTGTTACTGGAAGTGGCTGCTATTATCTTCTCTGATCC 299
QY 406 TGATCTCTGTTGGCTGAGCTACCCCTATGAACAACATGAATGCCATTTTCCAAATA 465
Db 300 TGATCTCTGTTGGCTGAGCTACCCCTATGAACAACATGAATGCCATTTTCCAAATA 359
QY 466 AAGCCATGCCCTCTGAGGAACACATTCCTTGGGTT 500
Db 360 AAGCCATGCCCTCTGAGGAACACATTCCTTGGGTT 394

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Search completed: April 3, 2003, 13:36:00  
 Job time : 91.2842 secs

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.7495 Seconds  
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Title: US-09-595-526C-1\_COPY\_1\_500  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description       |
|------------|-------|-------|--------|----|-------------------|
| 1          | 34.2  | 6.8   | 12537  | 2  | US-08-611-280-4   |
| 2          | 34.2  | 6.8   | 12537  | 4  | US-09-195-940-4   |
| 3          | 34.2  | 6.8   | 12537  | 4  | US-09-562-466-4   |
| 4          | 31.4  | 6.3   | 111282 | 4  | US-09-754-250-3   |
| 5          | 31.2  | 6.2   | 1006   | 4  | US-08-988-242-17  |
| 6          | 30.6  | 6.1   | 733    | 4  | US-09-082-092-15  |
| 7          | 30.6  | 6.1   | 2875   | 3  | US-08-458-434A-4  |
| 8          | 30.6  | 6.1   | 14636  | 4  | US-09-173-914-6   |
| 9          | 30.2  | 6.0   | 454    | 4  | US-08-998-416-84  |
| 10         | 30.2  | 6.0   | 1835   | 4  | US-09-483-549-1   |
| 11         | 30.2  | 6.0   | 6525   | 3  | US-08-762-500-74  |
| 12         | 29.8  | 6.0   | 5097   | 4  | US-09-315-793-11  |
| 13         | 29.6  | 5.9   | 987    | 4  | US-09-370-838-289 |
| 14         | 29.6  | 5.9   | 1146   | 1  | US-08-482-385A-1  |
| 15         | 29.6  | 5.9   | 2728   | 1  | US-08-482-385A-5  |
| 16         | 29.4  | 5.9   | 2067   | 2  | US-08-713-928B-8  |
| 17         | 29.4  | 5.9   | 2155   | 3  | US-09-191-171-4   |
| 18         | 29.4  | 5.9   | 2155   | 4  | US-09-385-707-4   |
| 19         | 29.4  | 5.9   | 2699   | 3  | US-09-167-354-5   |
| 20         | 29.4  | 5.9   | 2699   | 4  | US-09-642-855-5   |
| 21         | 29.4  | 5.9   | 2699   | 4  | US-09-642-514-5   |
| 22         | 29.4  | 5.9   | 3627   | 2  | US-08-232-087A-1  |
| 23         | 29.4  | 5.9   | 4480   | 3  | US-09-191-171-7   |
| 24         | 29.4  | 5.9   | 4480   | 4  | US-09-385-707-7   |
| 25         | 29.4  | 5.9   | 6200   | 4  | US-09-439-923-1   |
| 26         | 29.2  | 5.8   | 4338   | 1  | US-08-015-986A-1  |
| 27         | 29.2  | 5.8   | 4338   | 2  | US-08-446-363-1   |

|    |      |     |         |   |                    |                    |
|----|------|-----|---------|---|--------------------|--------------------|
| 28 | 29   | 5.8 | 1299    | 3 | US-08-793-035-3    | Sequence 3, Appli  |
| 29 | 29   | 5.8 | 2754    | 4 | US-09-429-322-3    | Sequence 3, Appli  |
| 30 | 29   | 5.8 | 3511    | 4 | US-09-453-702B-187 | Sequence 187, App  |
| 31 | 29   | 5.8 | 6176    | 3 | US-08-911-321-6    | Sequence 6, Appli  |
| 32 | 28.8 | 5.8 | 1633    | 4 | US-09-119-788-1    | Sequence 1, Appli  |
| 33 | 28.8 | 5.8 | 30001   | 1 | US-08-125-468-1    | Sequence 1, Appli  |
| 34 | 28.8 | 5.8 | 30051   | 2 | US-08-474-933-1    | Sequence 1, Appli  |
| 35 | 28.8 | 5.8 | 168575  | 4 | US-09-426-290-1    | Sequence 1, Appli  |
| 36 | 28.8 | 5.8 | 4403765 | 4 | US-09-103-840A-2   | Sequence 2, Appli  |
| 37 | 28.8 | 5.8 | 4411529 | 4 | US-09-103-840A-1   | Sequence 1, Appli  |
| 38 | 28.6 | 5.7 | 599     | 6 | 5430019-1          | Patent No. 5430019 |
| 39 | 28.6 | 5.7 | 2180    | 2 | US-08-755-559-2    | Sequence 2, Appli  |
| 40 | 28.6 | 5.7 | 2180    | 3 | US-09-210-474-2    | Sequence 2, Appli  |
| 41 | 28.6 | 5.7 | 2180    | 4 | US-09-539-774-2    | Sequence 2, Appli  |
| 42 | 28.6 | 5.7 | 2326    | 4 | US-09-154-750A-76  | Sequence 76, Appli |
| 43 | 28.6 | 5.7 | 15378   | 3 | US-08-785-420-1    | Sequence 1, Appli  |
| 44 | 28.4 | 5.7 | 4771    | 2 | US-08-866-650-2    | Sequence 2, Appli  |
| 45 | 28.4 | 5.7 | 4771    | 2 | US-09-021-287-2    | Sequence 2, Appli  |

ALIGNMENTS

RESULT 1  
US-08-611-280-4  
; Sequence 4, Application US/08611280  
; Patent No. 5891666  
; GENERAL INFORMATION:  
; APPLICANT: Matsuyama, Toshifumi  
; APPLICANT: Grossman, Alex  
; APPLICANT: Richardson, Christopher D.  
; TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Angen Canada Inc.  
; STREET: 6733 Mississauga Road, Suite 303  
; CITY: Mississauga  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: L5N 6J8  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,280  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oleski, Nancy A.  
; REGISTRATION NUMBER: 34,688  
; REFERENCE/DOCKET NUMBER: A-338A  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12537 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-611-280-4

|                       |        |  |       |                                  |
|-----------------------|--------|--|-------|----------------------------------|
| Query Match           | 6.8%;  | Score 34.2;  | DB 2; | Length 12537;                    |
| Best Local Similarity | 55.5%; | Pred. No. 1.2;   |       |                                  |
| Matches               | 66;    | Conservative   | 0;    | Mismatches 53; Indels 0; Gaps 0; |
| QY                    | 296    | TTGTTGGCTCAGCGAGGTTGCTGCTGGAAGAACCTCACTTTCAGGAAGAAACAAC    | 355   |                                  |
| Db                    | 22     | TTGTCGCTCAGCTAGTAAGAGTCGGGTGAGTAGGCTGTAGTCGGCAGAGGAGGAG    | 81    |                                  |
| QY                    | 356    | ATGTCAGCTGTACAGAGTGCGCTCGCCCTATTTATCTTCCTGATCCTGATCTG      | 414   |                                  |
| Db                    | 82     | TGTGAGGCTGCTGGCAGAGGAAGCCTGGCTTCATCTCTGAGCCTGAGGAGAGATGCTG | 140   |                                  |





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Db 38748 CCTCT 38744      | ||
                          ;
RESULT 5
US-08-988-242-17/C
; Sequence 17, Application US/08988242
; Patent No. 6403103
; GENERAL INFORMATION:
; APPLICANT: PARAMHOS-BACCALA, GLAUCIA
; APPLICANT: LESENECHAL, MYLENE
; APPLICANT: JOLIVET, MICHEL
; APPLICANT: MANDRAND, BERNARD
; TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, GENE
; TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
; TITLE OF INVENTION: CHAGAS DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,242
; FILING DATE: 10-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36400A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1006 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-988-242-17
Query Match          6.2%; Score 31.2; DB 4; Length 1006;
Best Local Similarity 55.6%; Pred. No. 2.9;
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 114 TTCCCCGGTTCCTGTTTCTCCCTTCTCGGAGGCCTGTCAAGGGGTAGGAGAAGACA 173
    |||||
Db 357 TCGGCCCTTCTCTCTCTCTCTCTTTCTCGCAAAATAATATAAAGGTGGAAACAAA 298
    |||||

Qy 174 CGCAACACAAAAGTGGAACACAGTTAATGACCACCCAGCGCCTCCC 221
    |||||||
Db 297 CACACACAAAAAAGAAAAAGAAAAAGAACAAATCTGACGCCTCCC 250
    |||||||

RESULT 6
US-09-082-092-15/C
; Sequence 15, Application US/09082092
; Patent No. 6251628
; GENERAL INFORMATION:
; APPLICANT: Nakao, Atsuhiro
; APPLICANT: Moren, Anita
; APPLICANT: Heuchel, Rainer
; APPLICANT: Itoh, Susumu
; APPLICANT: Afrakhte, Mozghan
; APPLICANT: Souchehlytskyi, Serhiy

; APPLICANT: Brodin, Greger
; APPLICANT: Landstrom, Marene
; APPLICANT: Heldin, Nils-Erik
; APPLICANT: Heldin, Carl-Henrik
; APPLICANT: ten Dijske, Peter
; TITLE OF INVENTION: SMAD7 AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,092
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,221
; FILING DATE: 20-MAY-1997
; APPLICATION NUMBER: 60/060,465
; FILING DATE: 30-SEP-1997
; APPLICATION NUMBER: 60/075,940
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: 60/077,033
; FILING DATE: 06-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-082-092-15
Query Match          6.1%; Score 30.6; DB 4; Length 733;
Best Local Similarity 60.0%; Pred. No. 3.8;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 217 GTCCCTGTGTGAGCTCTGGCGGCTTCCAGGGCTCCGAGCACACGCTGGCGGTG 276
    |||||
Db 717 GCGCCGCTGGGGGCTCGCGCGGACTCATGGGACTCGGGGSCCGAGCGCTCGCGCGC 658
    |||||

Qy 277 CTGGCTGAGGGAACATGCTGTGTTG 301
    |||||
Db 657 GTGGCCCGGCTGGCTGGCTGGCTG 633
    |||||

RESULT 7
US-08-458-434A-4
; Sequence 4, Application US/0845843A
; Patent No. 6083690
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Stephen E.
; APPLICANT: Mundy M.D., Gregory R.
; APPLICANT: Gosh-Choudhury Ph.D., Nandini
; APPLICANT: Feng Ph.D., Jian Q.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: OSTEOGENIC AGENTS
; NUMBER OF SEQUENCES: 13

```



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RESULT 12
US-09-315-793-11
; Sequence 11, Application US/09315793
; Patent No. 6221597
; GENERAL INFORMATION:
; APPLICANT: Roberts, Christopher J.
; TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
; TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 9301-048
; CURRENT APPLICATION NUMBER: US/09/315,793
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5097
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-315-793-11

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US-09-315-793-11
; Sequence 11, Application US/09315793
; Patent No 6231597
; GENERAL INFORMATION:
; APPLICANT: Roberts, Christopher J.
; TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
; TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
; TITLE OF INVENTION: DRUGS
; FILE REFERENCE: 9301-048
; CURRENT APPLICATION NUMBER: US/09/315,793
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5097
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-315-793-11

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11
RESULT 11
US-08-762-500-74
; Sequence 74, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996

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Db 3170 AGATTTCAC 3178

## RESULT 13

US-09-838-889/c  
; Sequence 289, Application US/09370838  
; Patent No. 644425

## GENERAL INFORMATION:

APPLICANT: Reed, Steven G.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Mohamath, Roadon  
APPLICANT: Heather  
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.475C1  
CURRENT APPLICATION NUMBER: US/09/370.838  
CURRENT FILING DATE: 1999-08-09  
EARLIER APPLICATION NUMBER: US 09/285.323  
EARLIER FILING DATE: 1999-04-02  
NUMBER OF SEQ ID NOS: 289  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 289  
LENGTH: 987  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-838-889-289

Query Match 5.9%; Score 29.6; DB 4; Length 987;  
Best Local Similarity 53.4%; Pred. No. 9.2;  
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 51 GCAGGGGGGAGCTCGCGGACCAAGAGCGGTCTCAGGGCGGTTCGTCCTGTGT 110

Db 468 GAAGATGGGGCAAGAGATCAGCTCCCGCGCTGTTCGCCCGCGGTTCCTCTT 409

QY 111 TTTTCCCGGTTCTGTTTCTCCGGAAGGCTTGTCAAGGGGTAGGAG 166

Db 408 TCCTCTCTTGTCTCAGCTCCCGCTGTCCCTCAGCTCCAGAGTAGGGAGGG 353

## RESULT 14

US-08-482-385A-1/c  
; Sequence 1, Application US/08482385A  
; Patent No. 5728561

## GENERAL INFORMATION:

APPLICANT: DENOVA,, CLAUDIO D.  
TITLE OF INVENTION: GENES ENCODING BRANCHED CHAIN ALPHA  
TITLE OF INVENTION: KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES  
NUMBER OF SEQUENCES: 15  
CURRENT APPLICATION DATA:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PETER C. RICHARDSON  
STREET: 235 EAST 42ND STREET, 20TH FLOOR  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A  
ZIP: 10017-5755

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482.385A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SHEYKA,, ROBERT F.  
REGISTRATION NUMBER: 31,304  
REFERENCE/DOCKET NUMBER: PC8346C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-573-1189  
TELEFAX: 212-573-1939  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1146 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-482-385A-1

Query Match 5.9%; Score 29.6; DB 1; Length 1146;  
Best Local Similarity 56.0%; Pred. No. 9.9;  
Matches 56; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 212 CGGGCGTCCCTGCTGTGAGCTCTGGCGGCTCTCCAGGCTCCGAGCCACACGCTGG 271

Db 224 CGGCCCTGCTGTGTGAGAGCGGTGCTGCTGTGTAGCGGGCGGCGCACCACTCC 165

QY 272 GCGTGTGCTGAGGGAACATGGCTTGTGGCCTCAGCTG 311

Db 164 GCGTACAGCGCGGCGCAGCAGTAGCGGTGCGCTCCGCGG 125

## RESULT 15

US-08-482-385A-5/c  
; Sequence 5, Application US/08482385A  
; Patent No. 5728561  
GENERAL INFORMATION:

APPLICANT: DENOVA,, CLAUDIO D.  
TITLE OF INVENTION: GENES ENCODING BRANCHED CHAIN ALPHA  
TITLE OF INVENTION: KETOACID DEHYDROGENASE FROM STREPTOMYCES SPECIES  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PETER C. RICHARDSON  
STREET: 235 EAST 42ND STREET, 20TH FLOOR  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A  
ZIP: 10017-5755  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482.385A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SHEYKA,, ROBERT F.  
REGISTRATION NUMBER: 31,304  
REFERENCE/DOCKET NUMBER: PC8346C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-573-1189  
TELEFAX: 212-573-1939  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2728 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-482-385A-5

Query Match 5.9%; Score 29.6; DB 1; Length 2728;  
Best Local Similarity 56.0%; Pred. No. 16;  
Matches 56; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 212 CGGGCGTCCCTGCTGTGAGCTCTGGCGGCTCTCCAGGCTCCGAGCCACACGCTGG 271

Db 626 CGGCCCTGCTGTGTGAGAGCGGTGCTGCTGTGTAGCGGGCGGCGCACCACTCC 567

QY 272 GCGTGTGCTGAGGGAACATGGCTTGTGGCCTCAGCTG 311

Db 566 GCGTACAGCGCGGCGCAGCAGTAGCGGTGCGCTCCGCGG 527

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 16:38:15 ; Search time 31.629 Seconds  
(without alignments)  
13866.500 Million cell updates/sec

Title: US-09-595-526C-1\_COPY\_1\_500  
Perfect score: 500  
Sequence: 1 ggcgggagccgagagccg.....caggaaacactcttgggtt 500

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description       |
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| 1          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-93  |
| 2          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-94  |
| 3          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-95  |
| 4          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-96  |
| 5          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-97  |
| 6          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-98  |
| 7          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-99  |
| 8          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-100 |
| 9          | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-101 |
| 10         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-102 |
| 11         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-103 |
| 12         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-104 |
| 13         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-105 |
| 14         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-106 |
| 15         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-107 |
| 16         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-108 |
| 17         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-109 |
| 18         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-110 |
| 19         | 483.2 | 95.6          | 9870   | 9     | US-09-984-827-111 |

#### ALIGNMENTS

RESULT 1  
US-09-984-827-93  
; Sequence 93. Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984.827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 93  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-93

|    |       |      |      |    |                    |                   |
|----|-------|------|------|----|--------------------|-------------------|
| 20 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-112  | Sequence 112, App |
| 21 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-113  | Sequence 113, App |
| 22 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-114  | Sequence 114, App |
| 23 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-115  | Sequence 115, App |
| 24 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-116  | Sequence 116, App |
| 25 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-117  | Sequence 117, App |
| 26 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-118  | Sequence 118, App |
| 27 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-119  | Sequence 119, App |
| 28 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-120  | Sequence 120, App |
| 29 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-121  | Sequence 121, App |
| 30 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-122  | Sequence 122, App |
| 31 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-123  | Sequence 123, App |
| 32 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-124  | Sequence 124, App |
| 33 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-125  | Sequence 125, App |
| 34 | 483.2 | 96.6 | 9870 | 9  | US-09-984-827-126  | Sequence 126, App |
| 35 | 481.6 | 96.3 | 9870 | 9  | US-09-984-827-92   | Sequence 92, Appl |
| 36 | 378.2 | 75.6 | 9741 | 9  | US-09-984-827-1    | Sequence 1, Appl  |
| 37 | 378.2 | 75.6 | 9741 | 10 | US-09-846-456-10   | Sequence 10, Appl |
| 38 | 289.2 | 57.8 | 1062 | 9  | US-09-924-340-101  | Sequence 101, App |
| 39 | 289.2 | 57.8 | 1062 | 9  | US-09-992-600A-101 | Sequence 101, App |
| 40 | 199.4 | 39.9 | 3231 | 9  | US-09-984-827-3    | Sequence 3, Appl  |
| 41 | 199.4 | 39.9 | 3231 | 10 | US-09-846-456-1    | Sequence 1, Appl  |
| 42 | 197   | 39.4 | 221  | 10 | US-09-846-456-4    | Sequence 4, Appl  |
| 43 | 195.4 | 39.1 | 221  | 9  | US-09-984-827-24   | Sequence 24, Appl |
| 44 | 159.4 | 31.9 | 357  | 9  | US-09-984-827-4    | Sequence 4, Appl  |
| 45 | 159.4 | 31.9 | 357  | 10 | US-09-846-456-2    | Sequence 2, Appl  |

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 1 GGCGGGACCGCAGAGCCGACCTCTCTCCGGGCTCGCGCAGGCGAGGGCGG 60  
Db 25 GGCGGGACCGCAGAGCCGACCTCTCTCCGGGCTCGCGCAGGCGAGGGCGG 84  
Qy 61 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGCGCTTTGCTCTGTTTTTCCCG 120  
Db 85 GGAGCTCCGCGCACCAACAGAGCCGGTTCTCAGGCGCTTTGCTCTGTTTTTCCCG 144

QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAAC 180  
Db 145 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACAGCCAGCGGCGTCCCTGTGTGAGCTCTGGCGGC 240  
Db 205 ACAAAGTGGAAACAGTTAATGACAGCCAGCGGCGTCCCTGTGTGAGCTCTGGCGGC 263  
QY 241 TGCCCTCCAGGCTCCGAGCCACAGCTGGCGTGTGAGGGAACATGCTTGT 300  
Db 264 TGCCCTCCAGGCTCCGAGCCACAGCTGGCGTGTGAGGGAACATGCTTGT 323  
QY 301 GGCCCTCAGCTGAGTGTGCTGTGGAAGAACCTCATTTCAGAGAAAGACAAACATGTC 360  
Db 324 GGCCCTCAGCTGAGTGTGCTGTGGAAGAACCTCATTTCAGAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCGTCTATTATCTTCCTGATCTGATCTCTGTTGGC 420  
Db 384 AGCTGTCTGGAAGTGGCGTCTATTATCTTCCTGATCTGATCTCTGTTGGC 443  
QY 421 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCG 480  
Db 444 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCG 503  
QY 481 CAGGAACACTTCCTTGGGT 500  
Db 504 CAGGAACACTTCCTTGGGT 523

## RESULT 2

US-09-984-827-94  
; Sequence 94, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984, 827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-94

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GCGCGGAGCCCGAGAGCCGAGCCGAGCCCTTCTCTCCGGGCTGCGGAGGAGGCGG 60  
Db 25 GCGCGGAGCCCGAGAGCCGAGCCGAGCCCTTCTCTCCGGGCTGCGGAGGAGGCGG 84  
QY 61 GGAGCTCCGCGCACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTCTTTTCCCG 120  
Db 85 GGAGCTCCGCGCACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTCTTTTCCCG 144

QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAAC 180  
Db 145 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACAGCCAGCGGCGTCCCTGTGTGAGCTCTGGCGGC 240  
Db 205 ACAAAGTGGAAACAGTTAATGACAGCCAGCGGCGTCCCTGTGTGAGCTCTGGCGGC 263  
QY 241 TGCCCTCCAGGCTCCGAGCCACAGCTGGCGTGTGAGGGAACATGCTTGT 300  
Db 264 TGCCCTCCAGGCTCCGAGCCACAGCTGGCGTGTGAGGGAACATGCTTGT 323  
QY 301 GGCCCTCAGCTGAGTGTGCTGTGGAAGAACCTCATTTCAGAGAAAGACAAACATGTC 360  
Db 324 GGCCCTCAGCTGAGTGTGCTGTGGAAGAACCTCATTTCAGAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCGTCTATTATCTTCCTGATCTGATCTCTGTTGGC 420  
Db 384 AGCTGTCTGGAAGTGGCGTCTATTATCTTCCTGATCTGATCTCTGTTGGC 443  
QY 421 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCG 480  
Db 444 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCG 503  
QY 481 CAGGAACACTTCCTTGGGT 500  
Db 504 CAGGAACACTTCCTTGGGT 523

## RESULT 3

US-09-984-827-95  
; Sequence 95, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984, 827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-95

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GCGCGGAGCCCGAGAGCCGAGCCGAGCCCTTCTCTCCGGGCTGCGGAGGAGGCGG 60  
Db 25 GCGCGGAGCCCGAGAGCCGAGCCGAGCCCTTCTCTCCGGGCTGCGGAGGAGGCGG 84  
QY 61 GGAGCTCCGCGCACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTCTTTTCCCG 120  
Db 85 GGAGCTCCGCGCACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTCTTTTCCCG 144  
QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAAAC 180



Db 145 GTTCTGTTTTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACACCGGCGTCCCTGCTGTGAGCTCTGGCGGC 240  
Db 205 ACAAAGTGGAAACAGTTAATGACACCGCAC -GGCGTCCCTGCTGTGAGCTCTGGCGGC 263  
QY 241 TGCCTTCAGGGCTCCGAGCCACAGCTGGCGTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCTTCAGGGCTCCGAGCCACAGCTGGCGTGGCTGAGGGAACATGGCTTGT 323  
QY 301 GGCTCAGCTGAGTTCGCTGTGGAAGACCTCACTTTCAAGAAGACAAACATGTC 360  
Db 324 GGCTCAGCTGAGTTCGCTGTGGAAGACCTCACTTTCAAGAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCTCTATTTATCTTCTGATCTGCTGTGTCGGC 420  
Db 384 AGCTGTACTGGAAGTGGCTGGCTCTATTTATCTTCTGATCTGCTGTGTCGGC 443  
QY 421 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

## RESULT 4

US-09-984-827-96  
; Sequence 96, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEUFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-96

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GCGCGGACCCGAGAGCCGAGCCGCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 60  
Db 25 GCGCGGACCCGAGAGCCGAGCCGCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 84  
QY 61 GGAGCTCCCGGACCAACAGAGCCGCTTCTCAGGGGCTTGTCTCTGTTTTTCCCG 120  
Db 85 GGAGCTCCCGGACCAACAGAGCCGCTTCTCAGGGGCTTGTCTCTGTTTTTCCCG 144  
QY 121 GTTCTGTTTTTCTCCCTTCTCCGAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAC 180  
Db 145 GTTCTGTTTTTCTCCCTTCTCCGAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAC 204

Db 145 GTTCTGTTTTTCTCCCGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACACCGGCGTCCCTGCTGTGAGCTCTGGCGGC 240  
Db 205 ACAAAGTGGAAACAGTTAATGACACCGCAC -GGCGTCCCTGCTGTGAGCTCTGGCGGC 263  
QY 241 TGCCTTCAGGGCTCCGAGCCACAGCTGGCGTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCTTCAGGGCTCCGAGCCACAGCTGGCGTGGCTGAGGGAACATGGCTTGT 323  
QY 301 GGCTCAGCTGAGTTCGCTGTGGAAGACCTCACTTTCAAGAAGACAAACATGTC 360  
Db 324 GGCTCAGCTGAGTTCGCTGTGGAAGACCTCACTTTCAAGAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCTCTATTTATCTTCTGATCTGCTGTGTCGGC 420  
Db 384 AGCTGTACTGGAAGTGGCTGGCTCTATTTATCTTCTGATCTGCTGTGTCGGC 443  
QY 421 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

## RESULT 5

US-09-984-827-97  
; Sequence 97, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEUFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-97

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GCGCGGACCCGAGAGCCGAGCCGCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 60  
Db 25 GCGCGGACCCGAGAGCCGAGCCGCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 84  
QY 61 GGAGCTCCCGGACCAACAGAGCCGCTTCTCAGGGGCTTGTCTCTGTTTTTCCCG 120  
Db 85 GGAGCTCCCGGACCAACAGAGCCGCTTCTCAGGGGCTTGTCTCTGTTTTTCCCG 144  
QY 121 GTTCTGTTTTTCTCCCTTCTCCGAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAC 180  
Db 145 GTTCTGTTTTTCTCCCTTCTCCGAGGCTTGTCAAGGGGTAGGAGAAAGAGACGCAAC 204

|    |     |  |     |
|----|-----|--|-----|
| Qy | 181 | ACAAATGGAACACATTATGACCACGACGGGGTCCCTGCTGTGAGCTCTGGCCGC       | 240 |
| Db | 205 | ACAAAGTGGAAACACATTATGACCACGACAC - GGGTCCCTGCTGTGAGCTCTGGCCGC | 263 |
| Qy | 241 | TGCTTCCAGGGTCCCGAGCCACACGCTGGGGTGTGTGCTCAGGGAACATGGCTGT      | 300 |
| Db | 264 | TGCTTCCAGGGTCCCGAGCCACGCTGGGGTGTGTGCTCAGGGAACATGGCTGT        | 323 |
| Qy | 301 | GGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAACACAAACATGTC   | 360 |
| Db | 324 | GGCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAACACAAACATGTC   | 383 |
| Qy | 361 | AGCTGTACTGGAAGTGGCGTGGCCCTATTATATCTTCGTGATCTCTGTGTCGGC       | 420 |
| Db | 384 | AGCTGCTGCTGGAAGTGGCGTGGCCCTATTATATCTTCGTGATCTCTGTGTCGGC      | 443 |
| Qy | 421 | TGAGCTACCCACCGCTATGAAACACATGAATGCCATTTTCCAAATAAGGCATGCCCTCTG | 480 |
| Db | 444 | TGAGCTACCCACCGCTATGAAACACATGAATGCCATTTTCCAAATAAGGCATGCCCTCTG | 503 |

RESULT 7  
 US-09-984-827-99  
 ; Sequence 99, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFFE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984,827  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 50/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 99  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-99

|    | Query Match           | 96.6%   | Score 483.2        | DB 9     | Length 9870 |
|----|-----------------------|---|--------------------|----------|-------------|
|    | Best Local Similarity | 99.2%   | Pred. No. 7.5e-153 |          |             |
|    | Matches 496           | Conservative 0  | Mismatches 3       | Indels 1 | Gaps        |
| QY | 1                     | GGCGGGACCGCAGACGCGAGCCGCTCTCCGGGCTGGCGAGGCGGCGG           | 60                 |          |             |
| Db | 25                    | GGCGGGACCGCAGACGCGAGCCGCTCTCCGGGCTGGCGAGGCGGCGG           | 84                 |          |             |
| QY | 61                    | GGAGTCGCGCCACCAACAGAGCGGTTCTCAGGGCGTTTCTCTTGTGTTTTC       | 120                |          |             |
| Db | 85                    | GGAGTCGCGCCACCAACAGAGCGGTTCTCAGGGCGTTTCTCTTGTGTTTTC       | 144                |          |             |
| QY | 121                   | GTTCGTGTTTTCCTCCCTCTCCGGAGGCTTGTCAAGGGTAGGAGAAAGAGCGCAAC  | 180                |          |             |
| Db | 145                   | GTTCGTGTTTTCCTCCCTCTCCGGAGGCTTGTCAAGGGTAGGAGAAAGAGCGCAAC  | 204                |          |             |
| QY | 181                   | ACAAAAGTGGAAACAGTTAATGACCAGCAGCGGCGTCCCTGTGTGAGCTCTGGCGCG | 240                |          |             |

Db 205 ACAAAGTGGAAACAGTTAATGACAGCCAC -GGCGTCCCTGCTGTGAGCTCTGGCGC 263  
QY 241 TGCCTTCCAGGCTCCGAGCCACACGCTGGCGTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCTTCCAGGCTCCGAGCCACACGCTGGGGTGTGAGGGAACATGGCTTGT 323  
QY 301 GGCCTCAGCTGAGGTTGCTGTGGAAGAACCTCATTTCAGAGAAGACAAACATGTC 360  
Db 324 GGCCTCAGCTGAGGTTGCTGTGGAAGAACCTCATTTCAGAGAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCTCTATTATATCTTCCTGATCTCTCTTGGC 420  
Db 384 AGCTGTCTGGAAGTGGCTGGCTCTATTATATCTTCCTGATCTCTCTTGGC 443  
QY 421 TGAGTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

RESULT 8  
US-09-984-827-100  
; Sequence 100, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-100

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GSCCGGACCCGAGAGCCGACCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 60  
Db 25 GSCCGGACCCGAGAGCCGACCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 84  
QY 61 GGAGTCCCGCGCACCAACAGAGCCGTTCTCAGGGCGCTTTGCTCTCTTTTCCCG 120  
Db 85 GGAGTCCCGCGCACCAACAGAGCCGTTCTCAGGGCGCTTTGCTCTCTTTTCCCG 144  
QY 121 GTTCTGTTTTCTCCCTTCTCGGAGGCTTGTCAAGGGGTAGGAGAAGACGCAAC 180  
Db 145 GTTCTGTTTTCTCCCTTCTCGGAGGCTTGTCAAGGGGTAGGAGAAGACGCAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACAGCCAGCGGCTCCCTGCTGTGAGCTCTGGCGC 240

Db 205 ACAAAGTGGAAACAGTTAATGACAGCCAC -GGCGTCCCTGCTGTGAGCTCTGGCGC 263  
QY 241 TGCCTTCCAGGCTCCGAGCCACACGCTGGCGTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCTTCCAGGCTCCGAGCCACACGCTGGGGTGTGAGGGAACATGGCTTGT 323  
QY 301 GGCCTCAGCTGAGGTTGCTGTGGAAGAACCTCATTTCAGAGAAGACAAACATGTC 360  
Db 324 GGCCTCAGCTGAGGTTGCTGTGGAAGAACCTCATTTCAGAGAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCTCTATTATATCTTCCTGATCTCTCTTGGC 420  
Db 384 AGCTGTCTGGAAGTGGCTGGCTCTATTATATCTTCCTGATCTCTCTTGGC 443  
QY 421 TGAGTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

RESULT 9  
US-09-984-827-101  
; Sequence 101, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 101  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-101

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GSCCGGACCCGAGAGCCGACCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 60  
Db 25 GSCCGGACCCGAGAGCCGACCTTCTCTCCGGGCTGCGGAGGCGAGGCGG 84  
QY 61 GGAGTCCCGCGCACCAACAGAGCCGTTCTCAGGGCGCTTTGCTCTCTTTTCCCG 120  
Db 85 GGAGTCCCGCGCACCAACAGAGCCGTTCTCAGGGCGCTTTGCTCTCTTTTCCCG 144  
QY 121 GTTCTGTTTTCTCCCTTCTCGGAGGCTTGTCAAGGGGTAGGAGAAGACGCAAC 180  
Db 145 GTTCTGTTTTCTCCCTTCTCGGAGGCTTGTCAAGGGGTAGGAGAAGACGCAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACAGCCAGCGGCTCCCTGCTGTGAGCTCTGGCGC 240  
Db 205 ACAAAGTGGAAACAGTTAATGACAGCCAC -GGCGTCCCTGCTGTGAGCTCTGGCGC 263

QY 241 TGCCTTCCAGGCTCCCGAGCCACACGCTGGGCGTCTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCTTCCAGGCTCCCGAGCCACACGCTGGGCGTCTGGCTGAGGGAACATGGCTTGT 323  
QY 301 GGCCTCAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 360  
Db 324 GGCCTCAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTCTGATCCTGATCTCTGTTCGGC 420  
Db 384 AGCTGTCTGGAAGTGGCTGGCCCTCTATTATCTCTGATCCTGATCTCTGTTCGGC 443  
QY 421 TGAGCTACCCACCTTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

RESULT 10  
US-09-984-827-102  
; Sequence 102, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 102  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-102

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
QY 1 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 60  
Db 25 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 84  
QY 61 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 120  
Db 85 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 144  
QY 121 GTCCTGTTTCTCCCTTCTCCGGAAGGCTGTCAAGGGGTAGGAGAAAGACAAACATGTC 180  
Db 145 GTCCTGTTTCTCCCTTCTCCGGAAGGCTGTCAAGGGGTAGGAGAAAGACAAACATGTC 204  
QY 181 ACAAAAGTGAAGAAACAGTTAATGACCAAGCCAGCGGCTGCTGTGAGCTCTGGCCGC 240  
Db 205 ACAAAAGTGAAGAAACAGTTAATGACCAAGCCAGCGGCTGCTGTGAGCTCTGGCCGC 263

QY 241 TGCCTTCCAGGCTCCCGAGCCACACGCTGGGCGTCTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCTTCCAGGCTCCCGAGCCACACGCTGGGCGTCTGGCTGAGGGAACATGGCTTGT 323  
QY 301 GGCCTCAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 360  
Db 324 GGCCTCAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTCTGATCCTGATCTCTGTTCGGC 420  
Db 384 AGCTGTCTGGAAGTGGCTGGCCCTCTATTATCTCTGATCCTGATCTCTGTTCGGC 443  
QY 421 TGAGCTACCCACCTTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTTATGAACAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

RESULT 11  
US-09-984-827-103  
; Sequence 103, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 103  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-103

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 60  
Db 25 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 84  
QY 61 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 120  
Db 85 GGCCTGAGCTGAGGTGCTGTGTGGAAGAACCTCCTTTCAGAGAAAGACAAACATGTC 144  
QY 121 GTCCTGTTTCTCCCTTCTCCGGAAGGCTGTCAAGGGGTAGGAGAAAGACAAACATGTC 180  
Db 145 GTCCTGTTTCTCCCTTCTCCGGAAGGCTGTCAAGGGGTAGGAGAAAGACAAACATGTC 204  
QY 181 ACAAAAGTGAAGAAACAGTTAATGACCAAGCCAGCGGCTGCTGTGAGCTCTGGCCGC 240  
Db 205 ACAAAAGTGAAGAAACAGTTAATGACCAAGCCAGCGGCTGCTGTGAGCTCTGGCCGC 263  
QY 241 TGCCTTCCAGGCTCCCGAGCCACACGCTGGGCGTCTGGCTGAGGGAACATGGCTTGT 300

Db 264 TGCCTTCCAGGGCTCCGAGCCACACAGCTGGGGTGTCTGGCTGAGGAACATGGCTTGT 323  
QY 301 GGCTCAGCTGAGGTTGCTGTGTGGAAGAACTCACTTTCAAGAAAGACAAACATGTC 360  
Db 324 GGCTCAGCTGAGGTTGCTGTGTGGAAGAACTCACTTTCAAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTCTCTGATCCTGATCTCTGTTCGGC 420  
Db 384 AGCTGTCTGGAAGTGGCTGGCCCTCTATTATCTCTCTGATCCTGATCTCTGTTCGGC 443  
QY 421 TGAGTACCCACCCCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGTACCCACCCCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCCCTGGGTT 500  
Db 504 CAGGAACACTTCCCTGGGTT 523

RESULT 12  
US-09-984-827-104  
; Sequence 104, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 104  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-104

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GGCCGGGACCCGACAGCGGACCGACCCCTTCTCTCCGGGTGCGGCGAGGGCGGG 60  
Db 25 GGCCGGGACCCGACAGCGGACCGACCCCTTCTCTCCGGGTGCGGCGAGGGCGG 84  
QY 61 GGAGCTCCGGCGACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTTTTTCCTCCG 120  
Db 85 GGAGCTCCGGCGACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTTTTTCCTCCG 144  
QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAGGGGTAGGAGAAAGACGCAAC 180  
Db 145 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAGGGGTAGGAGAAAGACGCAAC 204  
QY 181 ACAAAAGTGAACAGTTAATGACAGCGGCGTCCCTGCTGTGTGAGCTCTGGCCGC 240  
Db 205 ACAAAAGTGAACAGTTAATGACAGCGCAC -GGCGTCCCTGCTGTGAGCTCTGGCCGC 263  
QY 241 TGCCCTCCAGGGCTCCGAGCCACAGCTGGGGTGTCTGGCTGAGGGAACATGGCTTGT 300

Db 264 TGCCTTCCAGGGCTCCGAGCCACACAGCTGGGGTGTCTGGCTGAGGAACATGGCTTGT 323  
QY 301 GGCTCAGCTGAGGTTGCTGTGTGGAAGAACTCACTTTCAAGAAAGACAAACATGTC 360  
Db 324 GGCTCAGCTGAGGTTGCTGTGTGGAAGAACTCACTTTCAAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACTGGAAGTGGCTGGCCCTCTATTATCTCTCTGATCCTGATCTCTGTTCGGC 420  
Db 384 AGCTGTCTGGAAGTGGCTGGCCCTCTATTATCTCTCTGATCCTGATCTCTGTTCGGC 443  
QY 421 TGAGTACCCACCCCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGTACCCACCCCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCCCTGGGTT 500  
Db 504 CAGGAACACTTCCCTGGGTT 523

RESULT 13  
US-09-984-827-105  
; Sequence 105, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 105  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-105

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GGCCGGGACCCGACAGCGGACCGACCCCTTCTCTCCGGGTGCGGCGAGGGCGGG 60  
Db 25 GGCCGGGACCCGACAGCGGACCGACCCCTTCTCTCCGGGTGCGGCGAGGGCGG 84  
QY 61 GGAGCTCCGGCGACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTTTTTCCTCCG 120  
Db 85 GGAGCTCCGGCGACCAACAGAGCGGTTCTCAGGGCGCTTGTCTCTTTTTCCTCCG 144  
QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAGGGGTAGGAGAAAGACGCAAC 180  
Db 145 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAGGGGTAGGAGAAAGACGCAAC 204  
QY 181 ACAAAAGTGAACAGTTAATGACAGCGGCGTCCCTGCTGTGTGAGCTCTGGCCGC 240  
Db 205 ACAAAAGTGAACAGTTAATGACAGCGCAC -GGCGTCCCTGCTGTGAGCTCTGGCCGC 263  
QY 241 TGCCCTCCAGGGCTCCGAGCCACAGCTGGGGTGTCTGGCTGAGGGAACATGGCTTGT 300  
Db 264 TGCCCTCCAGGGCTCCGAGCCACAGCTGGGGTGTCTGGCTGAGGGAACATGGCTTGT 323

QY 301 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 360  
Db 324 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACGTGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 420  
Db 384 AGCTGTGCTGGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 443  
QY 421 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

RESULT 14  
US-09-984-827-106  
; Sequence 106, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 106  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-106

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 360  
Db 25 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACGTGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 420  
Db 384 AGCTGTGCTGGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 443  
QY 421 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

QY 301 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 360  
Db 324 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACGTGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 420  
Db 384 AGCTGTGCTGGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 443  
QY 421 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

RESULT 15  
US-09-984-827-107  
; Sequence 107, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 107  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-107

Query Match 96.6%; Score 483.2; DB 9; Length 9870;  
Best Local Similarity 99.2%; Pred. No. 7.5e-153;  
Matches 496; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 360  
Db 25 GGCCTCAGCTGAGGTTCGCTGTGGAAGAACCTCCTTTTCAAGAAAGACAAACATGTC 383  
QY 361 AGCTGTACGTGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 420  
Db 384 AGCTGTGCTGGAAGTGGCTGGCCCTATTTATCTTCCGTGATCTGTCGTTCGGC 443  
QY 421 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCTTGGGTT 500  
Db 504 CAGGAACACTTCTTGGGTT 523

Db 324 GGCCTCAGCTGAGGTGCTGCTGTGGAGAACCTCACATTCAGAAGAAGACAACATGTC 383  
QY 361 AGCTGTTACTGGAGTGGCGCTCTATTATCTTCTGATCCTGATCCTGATCCTGTTGGC 420  
Db 384 AGCTGCTGCTGGAGTGGCGCTCTATTATCTTCTGATCCTGATCCTGTTGGC 443  
QY 421 TGAGCTACCCACCCCTATGAACAACATGAATGCCATTTCCAAATAAAGCCATGCCCTCTG 480  
Db 444 TGAGCTACCCACCCCTATGAACAACATGAATGCCATTTCCAAATAAAGCCATGCCCTCTG 503  
QY 481 CAGGAACACTTCCTTTGGGTT 500  
Db 504 CAGGAACACTTCCTTTGGGTT 523

Search completed: April 4, 2003, 06:41:22  
Job time : 42.629 secs





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OM nucleic - nucleic search, using sw model  
Run on: April 3, 2003, 09:40:44 ; Search time 565.192 Seconds  
(without alignments)  
14327.411 Million cell updates/sec

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Perfect score: 500  
Sequence: 1 ggcgggaccgcgagccg.....caggacacacttccttggtt 500

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estin:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hcc:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_hcc:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: gb\_gss:\*
  - 18: em\_gss\_hum:\*
  - 19: em\_gss\_inv:\*
  - 20: em\_gss\_pln:\*
  - 21: em\_gss\_vrt:\*
  - 22: em\_gss\_fun:\*
  - 23: em\_gss\_mam:\*
  - 24: em\_gss\_mus:\*
  - 25: em\_gss\_other:\*
  - 26: em\_gss\_pro:\*
  - 27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 485.8 | 97.2        | 547    | 9     | AL698654    |
| 2          | 481.6 | 96.3        | 736    | 9     | AU135588    |
| 3          | 268.4 | 53.7        | 292    | 14    | Z44377      |
| 4          | 264.8 | 53.0        | 619    | 10    | B8657864    |
| 5          | 254.8 | 51.0        | 535    | 12    | BG384217    |
| 6          | 199.4 | 39.9        | 763    | 9     | AU121731    |

|    |      |      |      |    |          |
|----|------|------|------|----|----------|
| 7  | 198  | 39.6 | 1004 | 11 | BC034824 |
| 8  | 178  | 35.6 | 998  | 12 | BG78861  |
| 9  | 100  | 20.0 | 575  | 13 | BI541694 |
| 10 | 92   | 18.4 | 335  | 10 | AW313960 |
| 11 | 88.6 | 17.7 | 470  | 17 | BH042929 |
| 12 | 87.2 | 17.4 | 370  | 14 | BM691885 |
| 13 | 87.2 | 17.4 | 522  | 9  | AL712499 |
| 14 | 87.2 | 17.4 | 523  | 9  | AL712388 |
| 15 | 87.2 | 17.4 | 562  | 9  | AL712461 |
| 16 | 85.6 | 17.1 | 462  | 9  | AL713392 |
| 17 | 85.6 | 17.1 | 492  | 9  | AL712362 |
| 18 | 82.2 | 16.4 | 315  | 12 | BF721282 |
| 19 | 73.4 | 14.7 | 259  | 10 | BB594265 |
| 20 | 73.4 | 14.7 | 272  | 10 | BB568993 |
| 21 | 68.6 | 13.7 | 365  | 10 | BB843149 |
| 22 | 67.4 | 13.5 | 276  | 10 | BB570397 |
| 23 | 65.8 | 13.2 | 547  | 17 | AZ769996 |
| 24 | 65.8 | 13.2 | 625  | 10 | BB65939  |
| 25 | 58.4 | 11.7 | 265  | 14 | BM940929 |
| 26 | 58   | 11.6 | 243  | 12 | BF455614 |
| 27 | 53.6 | 10.7 | 218  | 10 | BB594197 |
| 28 | 50.6 | 10.1 | 344  | 13 | BM149133 |
| 29 | 45.2 | 9.0  | 694  | 14 | BO597641 |
| 30 | 45   | 9.0  | 1054 | 13 | BM544515 |
| 31 | 41   | 8.2  | 533  | 10 | AV845237 |
| 32 | 40.8 | 8.2  | 914  | 17 | CNS03W8  |
| 33 | 40.2 | 8.0  | 520  | 10 | AV955395 |
| 34 | 39.4 | 7.9  | 571  | 10 | AV862022 |
| 35 | 39.4 | 7.9  | 694  | 13 | BI820797 |
| 36 | 39.4 | 7.9  | 758  | 13 | BI821177 |
| 37 | 39.4 | 7.9  | 824  | 13 | BI911609 |
| 38 | 39.4 | 7.9  | 916  | 14 | BM808544 |
| 39 | 39.4 | 7.9  | 986  | 13 | BI821324 |
| 40 | 39.4 | 7.9  | 1078 | 13 | BM548310 |
| 41 | 39.4 | 7.9  | 1129 | 14 | BM807409 |
| 42 | 39.4 | 7.9  | 1301 | 13 | BM548343 |
| 43 | 39.4 | 7.9  | 2065 | 11 | BC029282 |
| 44 | 38.6 | 7.7  | 541  | 14 | BM62914  |
| 45 | 38.6 | 7.7  | 564  | 10 | AV975288 |

ALIGNMENTS

RESULT 1  
AL698654  
LOCUS  
DEFINITION  
DKEZp686N12109\_x1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DKEZp686N12109 5', mRNA sequence.  
ACCESSION  
AL698654  
VERSION  
AL698654.1  
KEYWORDS  
GI:19619194  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 547)  
AUTHORS  
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann  
,S.  
EST (Duesterhoeft, et al.)  
Unpublished (1999)  
JOURNAL  
Contact: Duesterhoeft A  
COMMENT  
MIPS  
Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No s1 sequence available.  
This clone (DKEZp686N12109) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzdpg.de.

547 bp mRNA linear EST 21-MAR-2002  
DKEZp686N12109\_x1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DKEZp686N12109 5', mRNA sequence.

```

FEATURES          Location/Qualifiers
Source
1..547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ686N12109"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI;
cDNA-collection"
BASE COUNT      112 a 154 c 157 g 124 t
ORIGIN
Query Match      97.2%; Score 485.8; DB 9; Length 547;
Best Local Similarity 99.4%; Pred. No. 7.4e-123;
Matches 498; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1 GCGCGGACCCGAGAGCGGAGCGGACCTTCTCTCCGGGCTGGGCGAGGCGGCGG 60
Db 24 GCGCGGACCCGAGAGCGGAGCGGACCTTCTCTCCGGGCTGGGCGAGGCGGCGG 83
QY 61 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGGGCTTTGCTCTCTG -TTTTTTCCCG 119
Db 84 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGGGCTTTGCTCTCTG -TTTTTTCCCG 143
QY 120 GGTTCGTGTTTTCTCCCTTCTCCGGGAGGCTTGTCAAGGGGTAGGAGAAAGAGAGCGCAA 179
Db 144 GGTTCGTGTTTTCTCCCTTCTCCGGGAGGCTTGTCAAGGGGTAGGAGAAAGAGAGCGCAA 203
QY 180 CACAAAGTGGAAACAGTAATGACAGCGGCTTCTCAGGGGCTTTGCTCTGAGCTCTGGCGG 239
Db 204 CACAAAGTGGAAACAGTAATGACAGCGGCTTCTCAGGGGCTTTGCTCTGAGCTCTGGCGG 263
QY 240 CTGCGCTTCAGGGCTCCCGAGGACACAGCTGGGCTGGCTGGGCTAGGGAACATGCTGT 299
Db 264 CTGCGCTTCAGGGCTCCCGAGGACACAGCTGGGCTGGCTGGGCTAGGGAACATGCTGT 323
QY 300 TGGCTTCAGCTGAGGTGCTGTGGGAGAACCTCAGCTTTTCCAGGAGAGAGAGAGAGAGAGT 359
Db 324 TGGCTTCAGCTGAGGTGCTGTGGGAGAACCTCAGCTTTTCCAGGAGAGAGAGAGAGAGT 383
QY 360 CAGCTGTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATCTGCTGCTGG 419
Db 384 CAGCTGTCTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATCTGCTGCTGG 443
QY 420 CTGAGCTACCCACCTATGAGCAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCT 479
Db 444 CTGAGCTACCCACCTATGAGCAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCT 503
QY 480 GCAGGAACACTTCCCTGGGTT 500
Db 504 GCAGGAACACTTCCCTGGGTT 524

RESULT 2
AUI35588 LOCUS      736 bp mRNA linear EST 02-AUG-2002
DEFINITION      AUI35588 PLACE1 Homo sapiens cDNA clone PLACE1002437 5', mRNA
sequence.
ACCESSION      AUI35588
VERSION        AUI35588.1 GI:10996127
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 736)
AUTHORS        Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE          HRI human cDNA project
JOURNAL        Unpublished (2000)

```

```

COMMENT
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES          Location/Qualifiers
Source
1..736
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002437"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: pME18SFL3"
BASE COUNT      163 a 199 c 199 g 170 t
ORIGIN
Query Match      96.3%; Score 481.6; DB 9; Length 736;
Best Local Similarity 99.0%; Pred. No. 1e-121;
Matches 495; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 1 GCGCGGACCCGAGAGCGGAGCGGACCTTCTCTCCGGGCTGGGCGAGGCGGCGG 60
Db 25 GCGCGGACCCGAGAGCGGAGCGGACCTTCTCTCCGGGCTGGGCGAGGCGGCGG 84
QY 61 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGGGCTTTGCTCTCTG -TTTTTTCCCG 120
Db 85 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGGGCTTTGCTCTCTG -TTTTTTCCCG 144
QY 121 GTTCTGTTTTCTCCCTTCTCCGGGAGGCTTGTCAAGGGGTAGGAGAAAGAGAGCGAAAC 180
Db 145 GTTCTGTTTTCTCCCTTCTCCGGGAGGCTTGTCAAGGGGTAGGAGAAAGAGAGCGAAAC 204
QY 181 ACAAAAGTGGAAACAGTTAATGACAGCGGCTTCTCAGGGGCTTTGCTCTGAGCTCTGGCGG 240
Db 205 ACAAAAGTGGAAACAGTTAATGACAGCGGCTTCTCAGGGGCTTTGCTCTGAGCTCTGGCGG 263
QY 241 TGCCTTCCAGGGCTCCCGAGGCCACACGCTGGGCTGTGCTGAGGGAACATGGCTTGT 300
Db 264 TGCCTTCCAGGGCTCCCGAGGCCACACGCTGGGCTGTGCTGAGGGAACATGGCTTGT 323
QY 301 GGCTCAGCTGAGGTGCTGCTGTGGAGAACCTCAGCTTTTCCAGGAGAGAGAGAGAGAGTGC 360
Db 324 GGCCCCAGCTGAGGTGCTGCTGTGGAGAACCTCAGCTTTTCCAGGAGAGAGAGAGAGAGTGC 383
QY 361 AGCTGTTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATCTCTGTTCCGGC 420
Db 384 AGCTGCTGCTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATCTCTGTTCCGGC 443
QY 421 TGAGCTACCCACCTATGAGCAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 480
Db 444 TGAGCTACCCACCTATGAGCAACATGAATGCCATTTTCCAAATAAAGCCATGCCCTCTG 503
QY 481 CAGGAACACTTCCCTGGGTT 500
Db 504 CAGGAACACTTCCCTGGGTT 523

RESULT 3
AUI35588 LOCUS      736 bp mRNA linear EST 14-NOV-1994
DEFINITION      HSC12B081 normalized infant brain cDNA Homo sapiens cDNA clone
c-12b08, mRNA sequence.
ACCESSION      AUI35588
VERSION        AUI35588.1 GI:573506
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens

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BASE COUNT 126 a 185 c 173 g 134 t 1 Others  
ORIGIN

Query Match 53.0%; Score 264.8; DB 10; Length 619;  
Best Local Similarity 75.6%; Pred. No. 3.7e-62;  
Matches 384; Conservative 0; Mismatches 112; Indels 12; Gaps 4;

QY 1 GGCCGGGACCGCAGAGCGAGCCCTCTCTCCGGGTGCGGAGGCGAGCGGG 60  
DB 26 GGCCGGGACCGCAGAGCGAGCCCTCTCTCCGGGTGCGGAGGCGAGCGGG 84  
QY 61 GGAGCTCCGGCAGCAGAGCGGTTCTCAGGGGCTTTGCTCCTTTTTCCTCG 120  
DB 85 GCGCGGGACCGCGCAACACAGCGGGCTTGGGAGCTGCTGCTCCTCTTTCCTCC 144  
QY 121 GTTCTGTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGACGAAC 180  
DB 145 CACTTTTCTTCCCTTCTGGAAGGTTTGTGCAAGGGGTAGGAGAAACAGACTCAAC 204  
QY 181 ACAAAGTGGAAACAGTTAATGACAGCAGCGGCTCCCTGCTGTGAGCTCTGGCGC 240  
DB 205 AGCAAGTGGAAACAGTTAATGACAGCAGCAGCAGCTGCTGCTGCTGCTGCTG 263  
QY 241 TGCTTCCAGGGGTCGAGGACCA-----CGCTGGGCTGCTGCTGAGGGAACA 291  
DB 264 T-CCCTCCAGGGCTCTGAGCGCGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTG 322  
QY 292 TGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 351  
DB 323 TGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 382  
QY 352 AACATGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 411  
DB 383 AACATGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 442  
QY 412 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471  
DB 443 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 502  
QY 472 TGCCCTCTCAGGAACACTTCTTGGGT 499  
DB 503 TGCCCTCTCAGGAACACTTCTTGGGT 530

RESULT 5  
BG384217  
LOCUS 303216 MARC 1P1G Sus scrofa cDNA 5', mRNA linear EST 12-MAR-2001  
DEFINITION BG384217  
ACCESSION BG384217  
VERSION BG384217.1 GI:13308689  
KEYWORDS EST.  
SOURCE Pig.

ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 535)  
Fahrenkrug, S.C., Frenking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,  
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.  
and Keele, J.W.

Design and use of two pooled tissue normalized cDNA libraries for  
EST discovery in swine  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel.: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980404.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.  
PCR Primers

FORWARD: AGGAAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGACG  
Plasm: 90 row: G column: 13  
Seq primer: ATTAGGTGACACTATAG.  
Location/Qualifiers  
1. 535  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
/clone\_lib="MARC 1P1G"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; site 1: NotI; site 2: SalI;  
Library made from pooled tissue from day 11, 13, 15, 20,  
and 30 embryos."

FEATURES  
source 121 a 159 c 136 g 119 t  
BASE COUNT

Query Match 51.0%; Score 254.8; DB 12; Length 535;  
Best Local Similarity 76.8%; Pred. No. 2.1e-59;  
Matches 384; Conservative 0; Mismatches 92; Indels 24; Gaps 5;  
QY 13 CAGAGCGGAGCGGACCTCTCTCCGGGTGCGGAGGCGGAGGAGGAGGAGGAGG 72  
DB 6 CGGGGCTTGGAGGACCTCTCTCCCTGGCGAAGGTGGGCTGGACAGGGGTCTCGCGC 65  
QY 73 ACCAACAGAGCGGCTTCTCAGGGGCTTGTCTCCTCTGTTTTTCCCGGCTCTGTTTCT 132  
DB 66 TACCAGCGCGC-----CACAGCAATTTCTCAGGCACTTT-----GCTCTCTTCCCA 115  
QY 133 CCCCTTCCGGAAGGTTGTCAAGGGGTAGGAGAAAGAGACGCAACACAAAGTGGAA 192  
DB 116 CACTTCTCGGAGAGATTTTCAAGGGGAGGCGGCAAGAGACGCAACACAAAGTGGAA 175  
QY 193 AACAGTTAATGACGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252  
DB 176 AACAGTTAATGACGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 233  
QY 253 CTCCC-----GAGCCACACGCTG-----GGCGTGTGCTGCTGAGGAAACATGGCTTGT 300  
DB 234 GCTCCCGAGGAGGAGCCACAGCGAGCTGGTGTGGTGCCAGCTGAGGTAAACATGGCTTAT 293  
QY 301 GGCCTCAGCTGAGTGTGCTGCTGGAAGAACCTCAGCTTTCAAGAGAGACAAACATGTC 360  
DB 294 GGACTCACTGAGGTACTGCTGGAAGAACCTCAGCTTTCAAGAGAGACAAACATGTC 353  
QY 361 AGCTGTTACTGGAAGTGGCGCTCTATTATCTTCCTGATCCTGATCTGTTGTCGGC 420  
DB 354 AGCTGTTGCTGGAAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413  
QY 421 TGAGTACCCACCTATGACACACATGATGCTTTCCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 414 TGAGTACCCACCTATGACACACATGATGCTTTCCTGCTGCTGCTGCTGCTGCTGCT 473  
QY 481 CAGGAACACTTCTTGGGT 500  
DB 474 CAGGAACACTTCTTGGGT 493

RESULT 6  
AUI21731  
LOCUS AUI21731 MAMMA1 Homo sapiens cDNA clone MAMMA1000851 5', mRNA  
DEFINITION sequence.  
ACCESSION AUI21731  
VERSION AUI21731.1 GI:10936966  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 763)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,  
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and

TITLE  
JOURNAL  
COMMENT

Isogai, T.  
HRI human cDNA project  
Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix  
Research Institute; cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

FEATURES  
Source

1. .763  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="MAMMAL000851"  
/clone\_lib="MAMMAL"  
/tissue\_type="mammary gland"  
/note="Vector: pME18SFL3"  
BASE COUNT 137 a 205 c 260 g 158 t  
ORIGIN

Query Match 39.9%; Score 199.4; DB 9; Length 763;  
Best Local Similarity 99.5%; Pred. No. 3.4e-44;  
Matches 200; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGCGGACCGGACGAGCGGACCCCTCTCTCCGGGCTGCGGCGAGGCGG 60  
DB 23 GGCGGACCGGACGAGCGGACCCCTCTCTCCGGGCTGCGGCGAGGCGG 82  
QY 61 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGCGCTTGTCTCTTTTCCCG 120  
DB 83 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGCGCTTGTCTCTTTTCCCG 142  
QY 121 GTTCTGTTTCTCCCTCTCCGGAAGCTTGCAAGGGTAGGAGAAAGAGCGCAAC 180  
DB 143 GTTCTGTTTCTCCCTCTCCGGAAGCTTGCAAGGGTAGGAGAAAGAGCGCAAC 202  
QY 181 ACAAAGTGGAAACAGTTAA 201  
DB 203 ACAAAGTGGAAACAGTTAA 223

RESULT 7  
BC034824  
LOCUS BC034824 1004 bp mRNA linear HTC 26-JUL-2002  
DEFINITION Homo sapiens, clone IMAGE:4749735, mRNA.  
ACCESSION BC034824  
VERSION BC034824.1 GI:21961568  
KEYWORDS HTC.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1004)  
Srausberg, R.  
Direct Submission  
Submitted (24-JUL-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC

Web site: http://www.hqsc.bcm.tmc.edu/cdna/  
Contact: ang@bcm.tmc.edu  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAK Plate: 52 Row: d Column: 19  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 5915657  
This clone has the following problem: incomplete processing.

FEATURES  
Source

1. .1004  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4749735"  
/tissue\_type="Skin, squamous cell carcinoma"  
/clone\_lib="NCI\_CGAP\_Skn4"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6.ccdB"  
BASE COUNT 306 a 234 c 230 g 234 t  
ORIGIN

Query Match 39.6%; Score 198; DB 11; Length 1004;  
Best Local Similarity 100.0%; Pred. No. 7.9e-44;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGCGGACCGGACGAGCGGACCCCTCTCTCCGGGCTGCGGCGAGGCGG 60  
DB 9 GGCGGACCGGACGAGCGGACCCCTCTCTCCGGGCTGCGGCGAGGCGG 68  
QY 61 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGCGCTTGTCTCTTTTCCCG 120  
DB 69 GGAGCTCCGGGACCAACAGAGCGGTTCTCAGGCGCTTGTCTCTTTTCCCG 128  
QY 121 GTTCTGTTTCTCCCTCTCCGGAAGCTTGCAAGGGTAGGAGAAAGAGCGCAAC 180  
DB 129 GTTCTGTTTCTCCCTCTCCGGAAGCTTGCAAGGGTAGGAGAAAGAGCGCAAC 188  
QY 181 ACAAAGTGGAAACAGT 198  
DB 189 ACAAAGTGGAAACAGT 206

RESULT 8

BC02624760F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4749735 5',  
LOCUS BC02624760F1 998 bp mRNA linear EST 01-MAY-2001  
DEFINITION mRNA sequence.  
ACCESSION BC02624760F1  
VERSION BC02624760F1.1 GI:13910258  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 998)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10603 row: g column: 16  
High quality sequence stop: 860.  
Location/Qualifiers

FEATURES

## source

1. .998  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:4749735"  
 /clone\_lib="NCL\_CGAP\_Skn4"  
 /tissue\_type="squamous cell carcinoma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: skin; Vector: pCMV-SF016; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCL\_CGAP Library."

BASE COUNT 285 a 233 c 244 g 236 t

ORIGIN

Query Match 35.6%; Score 178; DB 12; Length 998;

Best Local Similarity 97.0%; Pred. No. 2.5e-38;

Matches 192; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 GGCGGACCGCCGAGCGCGGACCTCTCTCCGGCTGCGCGGCGGCGGCGGCGG 60

Db 7 GGCGGACCGCCGAGCGCGGACCTCTCTCCGGCTGCGCGGCGGCGGCGGCGG 66

QY 61 GGAGCTCCGCGCCACCAACAGAGCGGTTCTCAGGGGCTTCTCTCTTTTCCCG 120

Db 67 GGAGCTCCGCGCCACCAACAGAGCGGTTCTCAGGGGCTTCTCTCTTTTCCCG 125

QY 121 GTTCTGTTTCTCCCTTCTCCGAGGCTTCTCAAGGGGTAGGAGAAAGAGCGCAAC 180

Db 126 GTTCTGTTTCTCCCTTCTCCGAGGCTTCTCAAGGGGTAGGAGAAAGAGCGCAAC 185

QY 181 ACAAAGTGGAAACAGT 198

Db 186 ACAAAGTGGAAACAGT 203

RESULT 9

BI541694

LOCUS

DEFINITION 455529 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.

ACCESSION BI541694

VERSION BI541694.1 GI:15382806

KEYWORDS EST.

SOURCE

ORGANISM

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 575)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C., Bennett

, G.L., Heaton, M.P., Laegreid, W., Rohrer, G.A., Chitko-McKown, C.G.,

Perlea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and

Keeler, J.W.

Sequence evaluation of four pooled-tissue normalized bovine CDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smithemail.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCAGGCG

Plate: 121 row: M column: 24

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1. .575

source

/organism="Bos taurus"  
 /db\_xref="taxon:9613"  
 /clone\_lib="MARC 1BOV"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
 Library made from pooled tissue from lymph node, ovary,  
 fat, hypothalamus, and pituitary."

BASE COUNT 102 a 192 c 147 g 134 t

ORIGIN

Query Match 20.0%; Score 100; DB 13; Length 575;

Best Local Similarity 67.0%; Pred. No. 7.1e-17;

Matches 142; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 288 AACATGGCTTGTGGCTCAGCTGAGTGTGCTGTGGAAGACCTCCTTCAGAGCA 347

Db 70 ACCATGGCTTGTGGCTCAGCTGAGTGTGCTGTGGAAGATTCCTATATCGGAG 129

QY 348 AGACAAACATGTACGTCTTACTTGAAGTGGCTGCTTATTTATCTTCTGATCTG 407

Db 130 AGGCAGCGGATCCAACTCTTGTGGAGTTGTGGCGCTCTTCTTCTTCATCTG 189

QY 408 ATCTCTGTTCGCTGAGCTACCCACCTTATGACAAACATGATGCCATTTCCAAATAA 467

Db 190 GTGGCGGTTCGCCATTCCTCCACCCCTCAGCAGCAGTGAATGTCAATTTCCCAACAAG 249

QY 468 GCCATGCCCTCTGCGAGCAACACTTCTTTGGGT 499

Db 250 CGGCTGCCCTCAGCAGCAGCACCATCCCTTGGCT 281

RESULT 10

AW313960

LOCUS

DEFINITION 9668 MARC 2PTG Sus scrofa CDNA 5', mRNA sequence.

ACCESSION AW313960

VERSION AW313960.1 GI:6743216

KEYWORDS EST.

SOURCE

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 335)

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,

Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.

and Keeler, J.W.

Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smithemail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 20

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTCAGGCG

Plate: 8 row: F column: 18

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1. .335

/organism="Sus scrofa"

/db\_xref="taxon:9823"

/clone\_lib="MARC 2PTG"

/tissue\_type="pooled"

/lab\_host="DH10B"

/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;

Library made from pooled tissue from testis, ovary,

BASE COUNT 61 a 107 c 84 g 83 t  
ORIGIN  
Query Match 18.4%; Score 92; DB 10; Length 335;  
Best Local Similarity 64.6%; Pred. No. 1.2e-14;  
Matches 137; Conservative 0; Mismatches 75; Indels 0; Gaps 0;  
QY 288 AACATGGCTGTGGCTCAGCTGAGTGGCTGCTGTGGAAGAACTCCTACATTCAGAAGA 347  
DB 122 ACATGGCTTCTGGACACAGCTAAATGCTGCTTTGGAAGAATTTCTGTATCGCAGG 181  
QY 348 AGACAAACATGTCAGCTGTACTGGAAGTGGCTGCTTATTTATCTCTCTGATCTCTG 407  
DB 182 AGACACCGATCCAGCTCTTGGTGGAGTTGATGGCCCTCTCTCTCTCTCTCTCTCTG 241  
QY 408 ATCTCTGTGGCTGAGCTACCCACCTATGACACACATGAATGCCATTTTCCAAATAA 467  
DB 242 GTGGCGGTCCGCAATTCACACCCCTCGAGCAGCATGAATGCCACTTCTCCAAACAAG 301  
QY 468 GCCATGCCCTCTCGAGGAACATTCCTTGGGT 499  
DB 302 CCCTTCCTTCAGCCGCTACCATCCCTTGGCT 333  
RESULT 11  
BH042929  
LOCUS  
DEFINITION RPCI-24-285D18\_TV RPCI-24 Mus musculus genomic clone RPCI-24-285D18  
DNA sequence.  
ACCESSION BH042929  
VERSION BH042929.1 GI:14824511  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 470)  
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akimret, B., Levins, M.,  
Tsedaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,  
Russell, D., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-24  
Unpublished (1999)  
Other\_GSSs: RPCI-24-285D18.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-24. For BAC  
library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org). Clones may be purchased from BACPAC  
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end  
page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
Plate: 285 row: D column: 18  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers  
1. .470  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-24-285D18"  
/clone\_lib="RPCI-24"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/note="Vector: pTARBAC1; Site.1: BamHI; Site.2: BamHI;  
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
library was cloned in the pTARBAC1 cloning vector at the  
BamHI sites using MboI partially digested male C57BL/6J  
DNA."

BASE COUNT 118 a 95 c 123 g 134 t  
ORIGIN  
Query Match 17.7%; Score 88.6; DB 17; Length 470;  
Best Local Similarity 91.3%; Pred. No. 9.8e-14;  
Matches 94; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 357 TGTACGCTGTACTGGAAGTGGCTGCTTATTTATCTCTGATCCTGATCTCTGTT 416  
DB 308 TGTACGCTGTACTGGAAGTGGCTGCTTATTTATCTCTGATCCTGATCTCTGTA 367  
QY 417 CGGCTGAGCTACCCACCTATGAACACATGAATGCCAATTTTC 459  
DB 368 CCCTGAGTACCCACCTAGACACACATGAGTGTGAGTATC 410  
RESULT 12  
BM591885  
LOCUS  
DEFINITION UI-E-CL1-aeg-b-11-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone  
UI-E-CL1-aeg-b-11-0-UI 5', mRNA sequence.  
ACCESSION BM591885  
VERSION BM591885.1 GI:19005143  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 370)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
9704477  
Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: msoares@blue.weeg.uiowa.edu  
Tissue Procurement: Dr. Gregg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics ([www.resgen.com](http://www.resgen.com)).  
The following repetitive elements were found in this cDNA  
sequence: 373-413, >POY\_A#Simple\_repeat  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. 370  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="UI-E-CL1-aeg-b-11-0-UI"  
/clone\_lib="UI-E-CL1"  
/tissue\_type="human retina"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site.1: EcoR I; Site.2: Not I;  
UI-E-CL1 is a normalized cDNA library containing the  
following tissue(s): retina. The library was constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (gt)18 tail. The  
sequence tag for this library is CCGCG. This library was  
created for the program, Gene Discovery in the Visual





QY 444 CATGAATGCCATTTCACAAATAAGCCATGCCCTCTGCGAGGAACACTTCCTTGGGT 499  
|||||  
Db 200 CATGAATGCCATTTCACAAAGCGATGCCCTCGGCGAGGAATGCTGCCGTGGCT 255  
|||||

RESULT 15  
AL712461 562 bp mRNA linear EST 22-MAR-2002  
LOCUS DKFZp686D1889\_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone  
DEFINITION DKFZp686D1889 5', mRNA sequence.  
ACCESSION AL712461  
VERSION AL712461.1 GI:19695817  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 562)  
AUTHORS Koehrer,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.  
TITLE EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Koehrer K  
MIPS  
Am Klopferspitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@kiz- heidelberg.de;  
sequenced by BWFZ (Biomedical Research Center at the Charite,  
Berlin/Germany) within the cDNA sequencing consortium of the German  
Genome Project.  
No sl sequence available.  
This clone (DKFZp686D1889) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
location/Qualifiers  
1..562  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp686D1889"  
/clone\_lib="686 (synonym: hlcc3)"  
/tissue\_type="human skeletal muscle"  
/dev\_stage="adult"  
/lab\_host="DH103"  
/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

BASE COUNT 141 a 139 c 140 g 142 t  
ORIGIN

Query Match 17.4%; Score 87.2; DB 9; Length 562;  
Best Local Similarity 60.6%; Pred. No. 2.3e-13;  
Matches 143; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 264 CACGCTGGGGCTGCTGCTGAGGGAACATGCTTGTGGCTCAGCTGAGGTTCGTCGTG 323  
|||  
Db 54 CAATCTGGTCTCGTGTGGTCATTCATCGATGGGCTTCCTGAGACAGATACAGCTTTGCTC 113  
|||||

QY 324 TGAAGAAGCTCACTTTCAGAGAAGACAAACATGTCAGCTGTACTGGAAGTGGCCTGG 383  
|||||  
Db 114 TGAAGAAGCTGGACCTCGCGGAAAGCAAGAAAGATTTCGCTTGTGGTGAAGCTCGGTGG 173  
|||||

QY 384 CCTCTATTATCTTCCTGATCCTGATCTCTGTTGCGCTGAGCTACCCACCTATGACAA 443  
|||||  
Db 174 CCTTATCTTATTCTTGGTCTGATCTGTTAAGGAATGCCAACCCGCTCTACAGCCAT 233  
|||||

QY 444 CATGAATGCCATTTCACAAATAAGCCATGCCCTCTGCGAGGAACACTTCCTTGGGT 499  
|||||  
Db 234 CATGAATGCCATTTCACCAACAGCGGATGCCCTCAGCAGGAATGCTGCCGTGGCT 289  
|||||

\_\_\_\_\_

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 992.895 Seconds  
(without alignments)  
14684.987 Million cell updates/sec

Title: US-09-595-526C-1\_COPY\_2250\_2750

Perfect score: 501

Sequence: 1 gtgatcatcaaggccatcgt.....tggagggaagatggcttcaat 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

| GenEmbl.* |                 |  |  |  |
|-----------|-----------------|--|--|--|
| 1:        | gb.pa.*         |  |  |  |
| 2:        | gb.htg.*        |  |  |  |
| 3:        | gb.in.*         |  |  |  |
| 4:        | gb.om.*         |  |  |  |
| 5:        | gb.ov.*         |  |  |  |
| 6:        | gb.pat.*        |  |  |  |
| 7:        | gb.ph.*         |  |  |  |
| 8:        | gb.pl.*         |  |  |  |
| 9:        | gb.pr.*         |  |  |  |
| 10:       | gb.ro.*         |  |  |  |
| 11:       | gb.st.*         |  |  |  |
| 12:       | gb.sy.*         |  |  |  |
| 13:       | gb.un.*         |  |  |  |
| 14:       | gb.vi.*         |  |  |  |
| 15:       | em.ba.*         |  |  |  |
| 16:       | em.fun.*        |  |  |  |
| 17:       | em.hum.*        |  |  |  |
| 18:       | em.in.*         |  |  |  |
| 19:       | em.mu.*         |  |  |  |
| 20:       | em.om.*         |  |  |  |
| 21:       | em.or.*         |  |  |  |
| 22:       | em.ov.*         |  |  |  |
| 23:       | em.pat.*        |  |  |  |
| 24:       | em.ph.*         |  |  |  |
| 25:       | em.pl.*         |  |  |  |
| 26:       | em.ro.*         |  |  |  |
| 27:       | em.sts.*        |  |  |  |
| 28:       | em.un.*         |  |  |  |
| 29:       | em.vi.*         |  |  |  |
| 30:       | em.htg_hum.*    |  |  |  |
| 31:       | em.htg_inv.*    |  |  |  |
| 32:       | em.htg_other.*  |  |  |  |
| 33:       | em.htg_mus.*    |  |  |  |
| 34:       | em.htg_pln.*    |  |  |  |
| 35:       | em.htg_rtd.*    |  |  |  |
| 36:       | em.htg_mam.*    |  |  |  |
| 37:       | em.htg_vrt.*    |  |  |  |
| 38:       | em.sy.*         |  |  |  |
| 39:       | em.htgo_hum.*   |  |  |  |
| 40:       | em.htgo_mus.*   |  |  |  |
| 41:       | em.htgo_other.* |  |  |  |

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID        | Description        |
|------------|-------|---------------|--------|----|-----------|--------------------|
| 1          | 501   | 100.0         | 10442  | 6  | AX060713  | AX060713 Sequence  |
| 2          | 501   | 100.0         | 10442  | 6  | AX060892  | AX060892 Sequence  |
| 3          | 501   | 100.0         | 10442  | 9  | AF285167  | AF285167 Homo sapi |
| 4          | 501   | 100.0         | 10474  | 6  | AX060719  | AX060719 Sequence  |
| 5          | 501   | 100.0         | 10474  | 6  | AX060721  | AX060721 Sequence  |
| 6          | 501   | 100.0         | 10474  | 6  | AX060898  | AX060898 Sequence  |
| 7          | 501   | 100.0         | 10474  | 6  | AX060900  | AX060900 Sequence  |
| 8          | 499.4 | 99.7          | 6786   | 9  | AB055982  | AB055982 Homo sapi |
| 9          | 499.4 | 99.7          | 6880   | 9  | AX253450  | AX253450 Sequence  |
| 10         | 499.4 | 99.7          | 6880   | 9  | AX253452  | AX253452 Homo sapi |
| 11         | 499.4 | 99.7          | 7260   | 6  | AX025942  | AX025942 Sequence  |
| 12         | 499.4 | 99.7          | 7860   | 6  | AX025944  | AX025944 Sequence  |
| 13         | 499.4 | 99.7          | 9495   | 6  | AX059978  | AX059978 Sequence  |
| 14         | 499.4 | 99.7          | 9497   | 9  | AF165281  | AF165281 Homo sapi |
| 15         | 499.4 | 99.7          | 9497   | 9  | AF165281  | AF165281 Homo sapi |
| 16         | 499.4 | 99.7          | 9593   | 6  | AX059976  | AX059976 Sequence  |
| 17         | 499.4 | 99.7          | 9741   | 6  | AX127830  | AX127830 Sequence  |
| 18         | 499.4 | 99.7          | 9741   | 6  | AX139817  | AX139817 Sequence  |
| 19         | 499.4 | 99.7          | 9741   | 6  | AX351038  | AX351038 Sequence  |
| 20         | 499.4 | 99.7          | 9854   | 6  | AX127831  | AX127831 Sequence  |
| 21         | 499.4 | 99.7          | 9854   | 6  | AX139818  | AX139818 Sequence  |
| 22         | 488.4 | 97.5          | 7862   | 6  | AX135712  | AX135712 Sequence  |
| 23         | 414.6 | 82.8          | 7878   | 10 | MMABE1    | X75926 Mus musculu |
| 24         | 343.8 | 68.6          | 7074   | 5  | AF362377  | AF362377 Gallus ga |
| 25         | 225   | 44.9          | 6027   | 9  | AB055390  | AB055390 Homo sapi |
| 26         | 225   | 44.9          | 6588   | 9  | AF250238  | AF250238 Homo sapi |
| 27         | 225   | 44.9          | 6704   | 9  | AF328787  | AF328787 Homo sapi |
| 28         | 225   | 44.9          | 7795   | 6  | AX429481  | AX429481 Sequence  |
| 29         | 224   | 44.7          | 242    | 9  | HSATPCB04 | AF165285 Homo sapi |
| 30         | 224   | 44.7          | 7660   | 6  | AX059884  | AX059884 Sequence  |
| 31         | 224   | 44.7          | 9181   | 6  | AX127771  | AX127771 Sequence  |
| 32         | 224   | 44.7          | 9181   | 6  | AX139758  | AX139758 Sequence  |
| 33         | 224   | 44.7          | 129608 | 9  | AL353685  | AL353685 Human DNA |
| 34         | 224   | 44.7          | 149034 | 9  | AF275948  | AF275948 Homo sapi |
| 35         | 224   | 44.7          | 183999 | 6  | AX092589  | AX092589 Sequence  |
| 36         | 224   | 44.7          | 201144 | 9  | AF287262  | AF287262 Homo sapi |
| 37         | 223.4 | 44.6          | 6432   | 6  | AX320364  | AX320364 Sequence  |
| 38         | 223.4 | 44.6          | 6768   | 6  | AX320362  | AX320362 Sequence  |
| 39         | 222   | 44.3          | 222    | 6  | AX059901  | AX059901 Sequence  |
| 40         | 220.4 | 44.0          | 222    | 6  | AX127840  | AX127840 Sequence  |
| 41         | 220.4 | 44.0          | 222    | 6  | AX139827  | AX139827 Sequence  |
| 42         | 220.2 | 44.0          | 5669   | 6  | AX202220  | AX202220 Sequence  |
| 43         | 220.2 | 44.0          | 6522   | 6  | AX202218  | AX202218 Sequence  |
| 44         | 217.4 | 43.4          | 5762   | 6  | AX080462  | AX080462 Sequence  |
| 45         | 217.4 | 43.4          | 6607   | 6  | AX080493  | AX080493 Sequence  |

# ALIGNMENTS

| RESULT 1   | AX060713  | AX060713    | 10442 bp               | DNA | linear | PAT 22-JAN-2001 |
|------------|---|-------------|------------------------|-----|--------|-----------------|
| LOCUS      | AX060713  | Sequence 1  | from Patent WO0078972. |     |        |                 |
| DEFINITION | AX060713  | Sequence 1  | from Patent WO0078972. |     |        |                 |
| ACCESSION  | AX060713  | Sequence 1  | from Patent WO0078972. |     |        |                 |
| VERSION    | AX060713.1  | GI:12406103 |                        |     |        |                 |
| KEYWORDS   | human.  |             |                        |     |        |                 |
| SOURCE     | human.  |             |                        |     |        |                 |
| ORGANISM   | Homo sapiens  |             |                        |     |        |                 |
|            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |             |                        |     |        |                 |
|            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |             |                        |     |        |                 |
| REFERENCE  | 1 (bases 1 to 10442)  |             |                        |     |        |                 |
| AUTHORS    | Lawn, R.M., Wade, D. and Garvin, M.                               |             |                        |     |        |                 |
| TITLE      | Regulation with binding cassette transporter protein abcl         |             |                        |     |        |                 |
| JOURNAL    | Patent: WO 0078972-A 1 28-DEC-2000;                               |             |                        |     |        |                 |

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FEATURES
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Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 TTGGCCCTTTTTCAGAGCAGGAGCAGTGGAGTGCAGTGGAGACACCTGTTGAGAGTCTT 480
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RESULT 2
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LOCUS
DEFINITION
Sequence 1 from Patent WO0078971.
ACCESSION
AX060892
VERSION
AX060892.1 GI:12406270
KEYWORDS
human.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10442)
AUTHORS
Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE
Ap binding cassette transporter protein abcl polypeptides
JOURNAL
CV THERAPEUTICS, INC. (US)
SUBMITTED
06-JUL-2000
DISCOVERED
3172 Porter Drive, Palo Alto, CA 94304, USA
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/db_xref="taxon:9606"
BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN
Query Match 100.0%; Score 501; DB 6; Length 10442.

Best Local Similarity 100.0%; Pred. No. 1e-119;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACCGCTGAAGAGACCATCGGGATC 60
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QY 481 GTGGAGGAAGATGGCTTCAAT 501
Db 2730 GTGGAGGAAGATGGCTTCAAT 2750

RESULT 3
AF285167
LOCUS
DEFINITION
Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
ACCESSION
AF285167
VERSION
AF285167.1 GI:9755158
KEYWORDS
Homo sapiens.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10442)
AUTHORS
Schwartz,K., Lawn,R.M. and Wade,D.P.
TITLE
ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
regulated by LXR
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 10442)
AUTHORS
Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K.,
Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
TITLE
Direct Submission
JOURNAL
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
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Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 GATCCCAGCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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QY 241 TTCTGATTAGCACACCTCTCTCCAGAGCCAACTTGGCAGACAGCTTGGGGGATCATC 300
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| Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.                   |
| 1 (bases 1 to 10474)  |
| Lawl,R.M., Wade,D., Oram,J.F. and Garvin,M.                                   |
| Atp binding cassette transporter protein abcl polypeptides                    |
| Patent: WO 0078971-A 9 28-DEC-2000;   |
| CV THERAPEUTICS, INC. (US)  |
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| DB 2522 TTCTCTGATTAGCACACACTCTTCTCCAGAGCCAACCTGGCAGCAGCGCTGTGGGGGCATCATC 2581 |
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| DB 2642 ACATCAAGATCTTCGCTAGGCTGCTCTCTGCTGCTGCTTTGGGTTGGCTGTGAGTAC 2701        |
| QY 421 TTTGCCCTTTTTTGGAGGACAGGCGATTGGAGTGGCAGTGGGACAACTGTTTGAGAGTCT 480       |
| DB 2702 TTTGCCCTTTTTTGGAGGACAGGCGATTGGAGTGGCAGTGGGACAACTGTTTGAGAGTCT 2761     |
| QY 481 GTGGAGGAAGATGGCTTCAAT 501  |
| DB 2762 GTGGAGGAAGATGGCTTCAAT 2782  |
| RESULT 8  |
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| LOCUS AB055982 6786 bp mRNA linear PRI 18-AUG-2001                            |
| DEFINITION Homo sapiens mRNA for ABCA1, complete cds.                         |
| ACCESSION AB055982  |
| VERSION AB055982.1 GI:15212106  |
| KEYWORDS  |
| SOURCE Homo sapiens CDNA to mRNA.   |
| ORGANISM  |
| Homo sapiens  |
| Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;             |
| Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.                   |
| REFERENCE   |
| AUTHORS   |
| TITLE   |
| JOURNAL   |
| REFERENCE   |
| AUTHORS   |
| Ueda,K., Kioka,N. and Tanaka,A.R.   |
| 2 (bases 1 to 6786)   |
| Unpublished   |
| A new topological model of functional human ABCA1-Signal peptide              |
| cleaveage and glycosylation of a large extracellular domain                   |
| Kidera,A.,  |
| Sadanami,K.,  |
| Arakawa,R.,   |
| Amachi,T., Yokoyama,S. and Ueda,K.  |
| 1   |

|            |  |   |                            |
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| Db         | 2080   | CTGTGTGAGCGCTGGCCCTGCTAGTGGTCATCCTGAAAGTAGGAAACCTGCTGCCCTACAGT    | 2139                       |
| QY         | 181  | GATCCACGCGTGGTGTGTTGCTCTTCCTGCTGCCGTGTTTGGTGTGGTGACAACTCCTGCAGTGC | 240                        |
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| QY         | 241  | TTCCCTGATTAGCACACTCTTCTCCAGAGCCAACTCGGAGCAGCCTGTGGGGGCATCATC      | 300                        |
| Db         | 2200   | TTCCCTGATTAGCACACTCTTCTCCAGAGCCAACTCGGAGCAGCCTGTGGGGGCATCATC      | 2259                       |
| QY         | 301  | TACTTCACGCGTGTACTCGCCCTACGCTCCTGTGTGGCATGGCAGCACTACGTGGGCTTC      | 360                        |
| Db         | 2260   | TACTTCACGCGTGTACTCGCCCTACGCTCCTGTGTGGCATGGCAGCACTACGTGGGCTTC      | 2319                       |
| QY         | 361  | ACACTCAAGATCTTCGCTAGCGCTGCTCTCCTGTGGCTTTTGGGTGGTGTGAGTAC          | 420                        |
| Db         | 2320   | ACACTCAAGATCTTCGCTAGCGCTGCTCTCCTGTGGCTTTTGGGTGGTGTGAGTAC          | 2379                       |
| QY         | 421  | TTTGCCCTTTTGGAGGACAGGCGATTGGATGCGAGTGGGCAACCTGTTTGAGAGTCT         | 480                        |
| Db         | 2380   | TTTGCCCTTTTGGAGGACAGGCGATTGGATGCGAGTGGGCAACCTGTTTGAGAGTCT         | 2439                       |
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| Db         | 2440   | GTGGAGGAAGATGGCTTCAAT   | 2460                       |
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| LOCUS      | AX253450   | 6880 bp   | DNA linear PAT 10-OCT-2001 |
| DEFINITION | Sequence 1 from Patent WO0170810.  |   |                            |
| ACCESSION  | AX253450   |   |                            |
| VERSION    | AX253450.1   | GI:16073978   |                            |
| KEYWORDS   | human.   |   |                            |
| SOURCE     | Homo sapiens   |   |                            |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                                     |   |                            |
| AUTHORS    | 1 (bases 1 to 6880)  |   |                            |
| TITLE      | Schmitz G. and Bodzioch, M.  |   |                            |
| JOURNAL    | Apb binding cassette transporter 1 (abcl) gene polymorphisms and uses thereof for the diagnosis and treatment of lipid, cardiovascular or inflammatory disorders |   |                            |
| FEATURES   | Patent: WO 0170810-A 1 27-SEP-2001; Bayer Aktiengesellschaft (DE)  |   |                            |
| SOURCE     | Location/Qualifiers  |   |                            |
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|            | /db_xref="taxon:9606"  |   |                            |
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| Query Match               | 99.7%; | Score 499.4;   | DB 6;     | Length 6880; |
| Best Local Similarity     | 99.8%; | Pred. No. 2.6e-119;  |           |              |
| Matches 500; Conservative | 0;     | Mismatches 1;  | Indels 0; | Gaps 0;      |
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|                           |        |  |           |              |
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| QY                        | 181    | GAPCCAGCGTGGTGTGTTGCTCTCCCTGTCCGCTGTTTGCTGTGGTGACAATCCTGCAGTGC | 240       |              |
|                           |        |  |           |              |
| Dd                        | 2080   | GATCCAGCGTGGTGTGTTGCTCTCCCTGTCCGCTGTTTGCTGTGGTGACAATCCTGCAGTGC | 2139      |              |

|            |   |  |             |
|------------|---|--|-------------|
| Qy         | 241   | TTCTCGATTAGCACACTCTCTCCAGAGCCAAACCTGGCAGCAGCCTGTGGGGCATCATC  | 300         |
| Db         | 2140  | TTCTCGATTAGCACACTCTCTCCAGAGCCAAACCTGGCAGCAGCCTGTGGGGCATCATC  | 2199        |
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| Db         | 2200  | TACTTCACGCTGTACTCGCCCTACGTCCTGTGTGTGGCATGCAGGACTACGTGGGCTTC  | 2259        |
| Qy         | 361   | ACACTCAAGATCTTGGCTAGAGCTGCTCTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTAC   | 420         |
| Db         | 2260  | ACACTCAAGATCTTGGCTAGAGCTGCTCTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTAC   | 2319        |
| Qy         | 421   | TTTGCCCTTTTGGAGACAGGGCATTTGGAGTGCAGTGGGCAACCTGTTGAGAGTCTT  | 480         |
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| Qy         | 481   | GTGGAGGAAGATGGCTTCAAT  | 501         |
| Db         | 2380  | GTGGAGGAAGATGGCTTCAAT  | 2400        |
| RESULT     | 10  |  |             |
| LOCUS      | HSA012376   | 6880 bp  | linear mRNA |
| DEFINITION | Homo sapiens mRNA for ATP-binding cassette transporter-1 (ABC-1).   |  |             |
| ACCESSION  | AJ012376  |  |             |
| VERSION    | AJ012376.1  | GI:4128032   |             |
| KEYWORDS   | ABC-1 gene; ATP-binding cassette transporter-1.   |  |             |
| SOURCE     | human.  |  |             |
| ORGANISM   | Homo sapiens  |  |             |
| REFERENCE  | 1   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |             |
| AUTHORS    | Langmann,T., Klucken,J., Reil,M., Liebisch,G., Luciani,M.F., Chimini,G., Kaminski,W.E. and Schmitz,G.   |  |             |
| TITLE      | Molecular cloning of the human ATP-binding cassette transporter 1 (hABC1): evidence for sterol-dependent regulation in macrophages                                    |  |             |
| JOURNAL    | Biochem. Biophys. Res. Commun. 257 (1), 25-33 (1999)  |  |             |
| MEDLINE    | 99194549  |  |             |
| PUBMED     | 10092505  |  |             |
| REFERENCE  | 2   |  |             |
| AUTHORS    | Langmann,T., Klucken,J., Reil,M., Liebisch,G., Luciani,M.F., Chimini,G., Kaminski,W. and Schmitz,G.   |  |             |
| TITLE      | Molecular Cloning of the Human ATP-Binding Cassette Transporter 1 (hABC1): Evidence for Detergent-Dependent Regulation in Macrophages                                 |  |             |
| JOURNAL    | Proc. Natl. Acad. Sci. U.S.A. 97, 7987-7992 (2000)  |  |             |
| REFERENCE  | 3   | (bases 1 to 6880)  |             |
| AUTHORS    | Langmann,T.   |  |             |
| TITLE      | Direct Submission   |  |             |
| JOURNAL    | Submitted (11-NOV-1998) Langmann T., Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Franz-Josef-Strauss-Allee 11, 93053, GERMANY |  |             |

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         /map="9q22-31"
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         /db_xref="SWISS-PROT:O95477"
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```





| KEYWORDS                  | human.  |
|---------------------------|---|
| SOURCE                    | human sapiens   |
| ORGANISM                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                      |
| REFERENCE                 | 1 (bases 1 to 9495)   |
| AUTHORS                   | Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C., Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H. and Brewer,H.B. |
| TITLE                     | Nucleic acid and proteinic acids corresponding to human gene abcl   |
| JOURNAL                   | Patent: WO 0078970-A 96 28-DEC-2000;  |
| FEATURES                  | Avantis Pharma S.A. (FR)  |
| source                    | Location/Qualifiers   |
|                           | 1..9495   |
|                           | /organism="Homo sapiens"  |
|                           | /db_xref="taxon:9606"   |
| BASE COUNT                | 2599 a 2115 c 2216 g 2564 t 1 others  |
| ORIGIN                    |   |
| Query Match               | 99.7%; Score 499.4; DB 6; Length 9495;  |
| Best Local Similarity     | 99.8%; Pred. No. 2.6e-119;  |
| Matches 500; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;  |
| QY 1                      | GTGATCATCAAGGCATCGTGTATGAGAAGGAGCAGCGCTGAAGAGAGACATCGCGATC 60   |
| Db 1998                   | GTGATCATCAAGGCATCGTGTATGAGAAGGAGCAGCGCTGAAGAGAGACATCGCGATC 1997   |
| QY 61                     | ATGGGCTGGACACACGATACCTCGTTTACGTGGTTTCATTAGTCCTCATTCCTCTT 120  |
| Db 1958                   | ATGGGCTGGACACACGATACCTCTGTTTACGTGGTTTCATTAGTCCTCATTCCTCTT 2017  |
| QY 121                    | CTTGTGAGCGGTGCGCTGCTAGTGGTCATCTGAAGTTAGGAACCTGTCGCCATCAGT 180   |
| Db 2018                   | CTTGTGAGCGGTGCGCTGCTAGTGGTCATCTGAAGTTAGGAACCTGTCGCCATCAGT 2077  |
| QY 181                    | GATCCAGCGTGGTGTGTTGCTTCCTGTCGGTGTGTTGCTGTGFGTGAACCTGTCAGTGC 240   |
| Db 2078                   | GATCCAGCGTGGTGTGTTGCTTCCTGTCGGTGTGTTGCTGTGFGTGAACCTGTCAGTGC 2137  |
| QY 241                    | TTCTGTGATTAGCACACCTTCTCCAGAGCAACCTGCAGCAGCCTGTGGGGGCATCATC 300  |
| Db 2138                   | TTCTGTGATTAGCACACCTTCTCCAGAGCAACCTGCAGCAGCCTGTGGGGGCATCATC 2197   |
| QY 301                    | TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGCATGGCAGGACTACGTGGGGCTC 360   |
| Db 2198                   | TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGTGCATGGCAGGACTACGTGGGGCTC 2257  |
| QY 361                    | ACACTCAAGATCTCGTAGCCCTGCTCTCCCTGTGCTGTTGGGTTGGCTGTGAGTAC 420  |
| Db 2258                   | ACACTCAAGATCTCGTAGCCCTGCTCTCCCTGTGCTGTTGGGTTGGCTGTGAGTAC 2317   |
| QY 421                    | TTTGCCCTTTTTCAGGAGCAGGGCATTTGGAGTCAGTGGACACACCTGTTTGAGAGTCCI 480  |
| Db 2318                   | TTTGCCCTTTTTCAGGAGCAGGGCATTTGGAGTCAGTGGACACACCTGTTTGAGAGTCCI 2377   |
| QY 481                    | GTGGAGGAAGATGCCTCAAT 501  |
| Db 2378                   | GTGGAGGAAGATGCCTCAAT 2398   |
| RESULT 14                 |   |
| AX059973                  | AX059973 9497 bp DNA linear PAT 22-JAN-2001   |
| LOCUS                     |   |
| DEFINITION                | Sequence 91 from Patent WO0078970.  |
| ACCESSION                 | AX059973  |
| VERSION                   | AX059973.1 GI:12405631  |
| KEYWORDS                  | human.  |
| SOURCE                    | human.  |
| ORGANISM                  | Homo sapiens  |
| REFERENCE                 | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                      |
| AUTHORS                   | Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,   |



Db 1960 ATGGGCTGGACAACAGCATCCTCTGGTTAGCTGGTTCAATTAGTAGCCTCATTCCTCTT 2019  
QY 121 CTTGTGAGCGCTGGCCTGCTAGTGGTTCATCCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180  
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Db 2020 CTTGTGAGCGCTGGCCTGCTAGTGGTTCATCCCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2079  
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QY 181 GATCCAGCGTGGTGTGTTCTCTTCCTGTCGCCGTGTTGCTGGTGACAAATCCTGCAGTGC 240  
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Db 2080 GATCCAGCGTGGTGTGTTCTCTTCCTGTCGCCGTGTTGCTGGTGACAAATCCTGCAGTGC 2139  
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QY 241 TTCCTGATTAGCACACTCTTCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATC 300  
|||||  
Db 2140 TTCCTGATTAGCACACTCTTCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATC 2199  
|||||  
QY 301 TACTTCACGCTGACCTGCCCTACCTACCTGCTGTGGCATGGCAGGACTACCTGGGCTTC 360  
|||||  
Db 2200 TACTTCACGCTGACCTGCCCTACCTACCTGCTGTGGCATGGCAGGACTACCTGGGCTTC 2259  
|||||  
QY 361 ACACCTCAGATCTGCTAGCCTGCTCTCCTGCTGTGGCTTTGGGTTGGCTGTGAGTAC 420  
|||||  
Db 2260 ACACCTCAGATCTGCTAGCCTGCTCTCCTGCTGTGGCTTTGGGTTGGCTGTGAGTAC 2319  
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QY 421 TTTGCCCTTTTGGAGGAGCAGGCGCATTTGGAGTGCAGTGGGACAACTGTTTCAGAGTCT 480  
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QY 481 GTGGAGGAAGATGGCTTCAAT 501  
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Db 2380 GTGGAGGAAGATGGCTTCAAT 2400

Search completed: April 3, 2003, 21:53:29  
Job time : 1032.89 secs



PA (CVTH-) CV THERAPEUTICS INC.  
 XX Lawn RM, Wade D, Garvin M;  
 XX WPI; 2001-137812/14.  
 DR  
 XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 PT useful for the development of agents for the treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX  
 XX  
 PS Disclosure; Page 122-126; 215pp; English.  
 XX  
 XX The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 CC membranes and utilises ATP hydrolysis to transport a wide variety of  
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in  
 CC the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder  
 CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 CC localised to chromosome 9q22-q31. The ABC1 genes and proteins are  
 CC useful for developing pharmaceutical agents for the treatment of heart  
 CC disease and other disorders associated with hypercholesterolemia and  
 CC atherosclerosis. The genes are useful for developing screening assays to  
 CC screen for compounds that regulate the expression of genes associated  
 CC with cholesterol transport. The genes and proteins are also useful for  
 CC are also useful as diagnostic indicators of cardiovascular disease and  
 CC other disorders associated with hypercholesterolemia.  
 XX  
 XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;  
 SQ  
 Query Match 100.0%; Score 501; DB 22; Length 10442;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-137;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGATCATCAAGGGCATCTGTATGAGAGGAGGACGGCTGAAGAGACCATCGGGATC 60  
 DB 2250 GTGATCATCAAGGGCATCTGTATGAGAGGAGGACGGCTGAAGAGACCATCGGGATC 2309  
 QY 61 ATGGGCTGGACACAGCATCTCTGTTAGCTGGTTCATTAGTAGCTCTATCTCTCT 120  
 DB 2310 ATGGGCTGGACACAGCATCTCTGTTAGCTGGTTCATTAGTAGCTCTATCTCTCT 2369  
 QY 121 CTGTGAGCGCTGGCGCTAGTGTATCTCTGAGTGTAGGAACTCTGCGCCCTACAGT 180  
 DB 2370 CTGTGAGCGCTGGCGCTAGTGTATCTCTGAGTGTAGGAACTCTGCGCCCTACAGT 2429  
 QY 181 GATCCAGCGTGGTGTCT 240  
 DB 2430 GATCCAGCGTGGTGTCT 2489  
 QY 241 TTCTGATTAGCACACT 300  
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 DB 2550 TACTTCACGCTGACTGCT 2609  
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 QY 421 TTTGCGCTTTTGGAGCAGCGGCAATGAGTGCAGTGGGACACCTCTTTTCAGAGTCTT 480  
 DB 2670 TTTGCGCTTTTGGAGCAGCGGCAATGAGTGCAGTGGGACACCTCTTTTTCAGAGTCTT 2729  
 QY 481 GTGGAGGAGATGGCTTCAAT 501  
 DB 2730 GTGGAGGAGATGGCTTCAAT 2750  
 RESULT 2

AAF24702  
 ID AAF24702 standard; DNA; 10442 BP.  
 XX  
 AC AAF24702;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a human ABC1 polypeptide.  
 XX  
 KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX  
 OS Homo sapiens.  
 XX  
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 FT CDS 291..7076  
 FT /\*tag= a  
 FT /product= "ABC1 polypeptide"  
 XX  
 FN WO2000078971-A2.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 16-JUN-2000; 2000WO-US16591.  
 XX  
 PR 18-JUN-1999; 99US-0140264.  
 PR 14-SEP-1999; 99US-0153872.  
 PR 19-NOV-1999; 99US-0166573.  
 XX  
 PA (CVTH-) CV THERAPEUTICS INC.  
 PA (UNIV ) UNIV WASHINGTON.  
 XX  
 PI Lawn RM, Wade D, Oram JF, Garvin M;  
 XX  
 DR WPI; 2001-137811/14.  
 DR P-PSDB; AAB31365.  
 XX  
 PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
 PT polynucleotides and polypeptides, useful for treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX  
 PS Claim 3; Page 117-123; 21lpp; English.  
 XX  
 CC The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 CC membranes and utilises ATP hydrolysis to transport a wide variety of  
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in  
 CC the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder  
 CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 CC localised to chromosome 9q22-q31. The ABC1 genes and proteins are  
 CC useful for developing pharmaceutical agents for the treatment of heart  
 CC disease and other disorders associated with hypercholesterolemia and  
 CC atherosclerosis. The genes are useful for developing screening assays to  
 CC screen for compounds that regulate the expression of genes associated  
 CC with cholesterol transport. The genes and proteins are also useful for  
 CC are also useful as diagnostic indicators of cardiovascular disease and  
 CC other disorders associated with hypercholesterolemia.  
 XX  
 SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;  
 Query Match 100.0%; Score 501; DB 22; Length 10442;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-137;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGATCATCAAGGGCATCTGTATGAGAGGAGGACGGCTGAAGAGACCATCGGGATC 60  
 DB 2250 GTGATCATCAAGGGCATCTGTATGAGAGGAGGACGGCTGAAGAGACCATCGGGATC 2309  
 QY 61 ATGGGCTGGACACAGCATCTCTGTTAGCTGGTTCATTAGTAGCTCTATCTCTCTT 120







CC ATP hydrolysis to transport a wide variety of substrates across the  
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for are also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;  
Query Match 100.0%; Score 501; DB 22; Length 10474;  
Best Local Similarity 100.0%; Pred. No. 8.4e-137;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 181 GATCCAGCGTGGTGTTCCTGCTCGTCTGTTGCTGTGGTGAACCTTCCTGAGTGC 240  
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QY 241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGSCAGACGCTGTGGGGCATCATC 300  
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Db TACTTCAGCTGTACCTGCCCTAGCTCCTGTGTGTGTCATGAGGACGCTGAGTGCCTT 2641  
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Db ACACCTCAAGATCTTCGCTAGCTGCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2701  
QY 421 TTTCCCTTTTGGAGAGCGGGCATTTGGAGTGCAGTGGGACACACCTGTTGAGAGTCTT 480  
Db TTTCCCTTTTGGAGAGCGGGCATTTGGAGTGCAGTGGGACACACCTGTTGAGAGTCTT 2761  
QY 481 GTGGAGGAAGATGCTTCAAT 501  
Db GTGGAGGAAGATGCTTCAAT 2782  
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ID AAF24708 standard; DNA; 10474 BP.  
XX  
AC AAF24708;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 323..7108  
FT /\*tag= a  
FT /product= "defective ABC1 polypeptide"  
XX WO200078971-A2.  
XX 28-DEC-2000.  
XX 16-JUN-2000; 2000WO-US16591.  
XX 18-JUN-1999; 99US-0140264.  
XX 14-SEP-1999; 99US-0153872.  
XX 19-NOV-1999; 99US-0166573.  
XX (CVTH-) CV THERAPEUTICS INC.  
XX (UNIW ) UNIV WASHINGTON.  
XX Lawn RM, Wade D, Oram JF, Garvin M;  
XX WPI; 2001-137811/14.  
XX P-PSDB; AAB31367.  
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
XX polynucleotides and polypeptides, useful for treatment of heart disease  
XX and other disorders associated with hypercholesterolemia and  
XX atherosclerosis  
XX Claim 30; Page 165-172; 211pp; English.  
XX The present sequence encodes a human adenosine triphosphate (ATP)  
XX binding cassette protein (ABC) 1 polypeptide, and is isolated from  
XX a Tangier disease patient. ABC1 resides in cell membranes and utilises  
XX ATP hydrolysis to transport a wide variety of substrates across the  
XX plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
XX mobilisation of intracellular cholesterol stores. ABC1 is defective in  
XX Tangier disease, a genetic disorder characterised by abnormal  
XX HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
XX 9q22-9q31. The ABC1 genes and proteins are useful for developing  
XX disorders associated with hypercholesterolemia and atherosclerosis. The  
XX genes are useful for developing screening assays to screen for compounds  
XX that regulate the expression of genes associated with cholesterol  
XX transport. The genes and proteins are also useful for are also useful  
XX as diagnostic indicators of cardiovascular disease and other disorders  
XX associated with hypercholesterolemia.  
XX  
SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;  
Query Match 100.0%; Score 501; DB 22; Length 10474;  
Best Local Similarity 100.0%; Pred. No. 8.4e-137;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGGCTGAAGAGACCATGCGGATC 60  
Db GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGGCTGAAGAGACCATGCGGATC 2341  
QY 61 ATGGGCTGGACACACACATCTCTGTTAGCTGTTTATAGTACGCTTCCTCTT 120  
Db ATGGGCTGGACACACACATCTCTGTTAGCTGTTTATAGTACGCTTCCTCTT 2401  
QY 121 CTTGTAGCCCTGGCTGCTAGTGGTTCATCTCTGAAGTTAGGAACCTGCTGCCCTACAGT 180  
Db CTTGTAGCCCTGGCTGCTAGTGGTTCATCTCTGAAGTTAGGAACCTGCTGCCCTACAGT 2461  
QY 181 GATCCAGCGTGGTGTTCCTGCTCGTCTGTTGCTGTGGTGAACCTTCCTGAGTGC 240  
Db GATCCAGCGTGGTGTTCCTGCTCGTCTGTTGCTGTGGTGAACCTTCCTGAGTGC 2521  
QY 241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGSCAGACGCTGTGGGGCATCATC 300  
Db TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGSCAGACGCTGTGGGGCATCATC 2581





Homo sapiens.

05-FEB-2001; 2001WO-US03800.

03-FEB-2000; 2000US-0496914.  
27-APR-2000; 2000US-0560875.

(HYSE-) HYSEQ INC.

WPI; 2001-457740/49.  
P-PSDB; ABB11956.

P-PSDB; ABB11956.

Human proteins and DNA encoding

treating or ameliorating a me

e.g. arthritis and cancer -

Claim 1; Page 833-835; 1963pp

SEADITIONES APP10091 - APP10330

sequences ABB10961-ABB12330  
sequences ABA08225-ABA09574

invention also relates to vec

nucleotide of the invention, antibodies against the polypeptide

or polypeptides in a sample,

bind to polypeptides of the 1 polypeptides of the invention

giving an insight into their

potential therapeutic applications include various activities including

differentiation activities; s

haematopoiesis regulatory act

chemotactic or chemokinetic a

thrombolytic activities; rece-

involved in oncogenesis, cancer depending on their biological

the invention are useful for

conditions, e.g., by protein cancers, haematopoietic disorders.

cancers, hematopoietic disorders, chronic inflammatory

proliferative retinopathy, at

vascular growth. Polypeptides

repair (or nucleic acids encoded

healing (e.g., of burns, incisions, and wounds) and immunomodulatory activities may

bacterial and fungal infection

Polypeptides with growth factors

manipulate stem cells in culture

that can be used to augment or

may also be used in the diagnosis

screening techniques. The pres-

novel human polypeptide of the

Sequence 7086 BP; 1773 A; 1739

|  |  |   |
|--|--|---|
| Query Match  |  | 99.7%; Score 499.4; DB 22; Length 7086;                           |
| Best Local Similarity  |  | 99.8%; Pred. No. 2.le-136;  |
| Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |  |   |
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| DB   | 2263   | GTGATCATCAAGGGCATCGTGTATGAGAGAGGACGCGCTGAAGAGACCATGCGGATC 2322    |
| QY   | 61   | ATGGGCGCTGGACACAGCATACTCGTGTAGCTGTTTCATTTAGTAGCCTCATTCCTCTT 120   |
| DB   | 2323   | ATGGGCGCTGGACACAGCATACTCGTGTAGCTGTTTCATTTAGTAGCCTCATTCCTCTT 2382  |
| QY   | 121  | CTTTGAGGCGCTGGCTGCTAGTGTATCTGCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180   |
| DB   | 2383   | CTTTGAGGCGCTGGCTGCTAGTGTATCTGCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2442  |
| QY   | 181  | GATCCAGCGCTGGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240    |
| DB   | 2443   | GATCCAGCGCTGGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2502   |
| QY   | 241  | TTCTCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGACGCTGTGGGGGCATCATC 300   |
| DB   | 2503   | TTCTCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGACGCTGTGGGGGCATCATC 2562  |
| QY   | 301  | TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGGCATGCGAGACTACGTTGGCTTC 360     |
| DB   | 2563   | TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGGCATGCGAGACTACGTTGGCTTC 2622    |
| QY   | 361  | ACACTCAAGATCTTCGCTAGCCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420   |
| DB   | 2623   | ACACTCAAGATCTTCGCTAGCCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2682  |
| QY   | 421  | TTTGCCCTTTTGGAGGAGGAGGCGCATTTGAGTGCAGTGGGACAACTGTTTGGAGTCTCT 480  |
| DB   | 2683   | TTTGCCCTTTTGGAGGAGGAGGCGCATTTGAGTGCAGTGGGACAACTGTTTGGAGTCTCT 2742 |
| QY   | 481  | GTGGAGGAAGATGGCTTCAAT 501   |
| DB   | 2743   | GTGGAGGAAGATGGCTTCAAT 2763  |
| RESULT 11  |  |   |
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| ID   | AAK52667   | standard; cdNA; 7086 BP.  |
| XX   | AAK52667;  |   |
| AC   | AAK52667;  |   |
| XX   | AAK52667;  |   |
| DT   | 06-NOV-2001 (first entry)  |   |
| XX   | Human polynucleotide SEQ ID NO 2196.                                     |   |
| XX   | Human; cytokine; cell proliferation; cell differentiation; gene therapy; |   |
| KW   | vaccine; peptide therapy; stem cell growth factor; haematopoiesis;       |   |
| KW   | tissue growth factor; immunomodulatory; cancer; leukaemia;               |   |
| KW   | nervous system disorder; arthritis; inflammation; ss.                    |   |
| XX   | Homo sapiens.  |   |
| XX   | WO200157190-A2.  |   |
| PN   | 09-AUG-2001.   |   |
| PD   | 05-FEB-2001; 2001WO-0504098.   |   |
| XX   | 03-FEB-2000; 2000US-0496914.   |   |
| PR   | 27-APR-2000; 2000US-0560875.   |   |
| PR   | 20-JUN-2000; 2000US-0598075.   |   |
| PR   | 19-JUL-2000; 2000US-0620325.   |   |
| PR   | 01-SEP-2000; 2000US-0654936.   |   |
| PR   | 15-SEP-2000; 2000US-0663561.   |   |
| PR   | 20-OCT-2000; 2000US-0693325.   |   |
| PR   | 30-NOV-2000; 2000US-0728422.   |   |
| XX   |  |   |

|           |  |   |
|-----------|--|---|
| PA        | (HYSE-) HYSEQ INC.   |   |
| XX        | Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;           |   |
| PI        | Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;                  |   |
| PI        | Xue AJ, Yang Y, Wejhrman T, Goodrich R;                                    |   |
| XX        | WPI: 2001-476283/51.   |   |
| DR        | P-PSDB; AAM79534.  |   |
| XX        | Nucleic acids encoding polypeptides with cytokine-like activities,         |   |
| PT        | useful in diagnosis and gene therapy -                                     |   |
| XX        | Claim 1; Page 4558-4560; 6221pp; English.                                  |   |
| XX        | The invention relates to polynucleotides (AAK51456-AAK53435) and the       |   |
| CC        | encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to |   |
| CC        | cytokine, cell proliferation or cell differentiation or which may induce   |   |
| CC        | production of other cytokines in other cell populations. The               |   |
| CC        | polynucleotides and polypeptides are useful in gene therapy, vaccines or   |   |
| CC        | peptide therapy. The polypeptides have various cytokine-like activities,   |   |
| CC        | e.g. stem cell growth factor activity, haematopoiesis regulating           |   |
| CC        | activity, tissue growth factor activity, immunomodulatory activity and     |   |
| CC        | activin/inhibin activity and may be useful in the diagnosis and/or         |   |
| CC        | treatment of cancer, leukaemia, nervous system disorders, arthritis and    |   |
| CC        | inflammation.  |   |
| CC        | Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666      |   |
| CC        | (AAM80020) are omitted as the relevant pages from the sequence listing     |   |
| CC        | were missing at the time of publication.                                   |   |
| XX        | Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;                 |   |
| SQ        | Query Match  | 99.7%; Score 499.4; DB 22; Length 7086;                           |
|           | Best Local Similarity  | 99.8%; Pred. No. 2.le-136;  |
|           | Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;               |   |
| QY        | 1  | GTGATCATCAAGGGCATCGTGTATGAGAGAGGACGCGCTGAAGAGACCATGCGGATC 60      |
| DB        | 2263   | GTGATCATCAAGGGCATCGTGTATGAGAGAGGACGCGCTGAAGAGACCATGCGGATC 2322    |
| QY        | 61   | ATGGGCGCTGGACACAGCATACTCTGTTAGCTGTTTCATTTAGTAGCCTCATTCCTCTT 120   |
| DB        | 2323   | ATGGGCGCTGGACACAGCATACTCTGTTAGCTGTTTCATTTAGTAGCCTCATTCCTCTT 2382  |
| QY        | 121  | CTTTGAGGCGCTGGCTGCTAGTGTATCTGCTGAAGTTAGGAAACCTGCTGCCCTACAGT 180   |
| DB        | 2383   | CTTTGAGGCGCTGGCTGCTAGTGTATCTGCTGAAGTTAGGAAACCTGCTGCCCTACAGT 2442  |
| QY        | 181  | GATCCAGCGCTGGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240    |
| DB        | 2443   | GATCCAGCGCTGGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2502   |
| QY        | 241  | TTCTCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGACGCTGTGGGGGCATCATC 300   |
| DB        | 2503   | TTCTCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGACGCTGTGGGGGCATCATC 2562  |
| QY        | 301  | TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGGCATGCGAGACTACGTTGGCTTC 360     |
| DB        | 2563   | TACTTCACGCTGTACCTGCCCTACGTCCTGTGTGGCATGCGAGACTACGTTGGCTTC 2622    |
| QY        | 361  | ACACTCAAGATCTTCGCTAGCCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420   |
| DB        | 2623   | ACACTCAAGATCTTCGCTAGCCTGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2682  |
| QY        | 421  | TTTGCCCTTTTGGAGGAGGAGGCGCATTTGAGTGCAGTGGGACAACTGTTTGGAGTCTCT 480  |
| DB        | 2683   | TTTGCCCTTTTGGAGGAGGAGGCGCATTTGAGTGCAGTGGGACAACTGTTTGGAGTCTCT 2742 |
| QY        | 481  | GTGGAGGAAGATGGCTTCAAT 501   |
| DB        | 2743   | GTGGAGGAAGATGGCTTCAAT 2763  |
| RESULT 12 |  |   |

```

AAD21326
ID AAD21326 standard; DNA; 7260 BP.
XX
AC AAD21326;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human ATP binding cassette transporter 1 (ABCL1) gene.
XX
KW Human: ATP binding cassette transporter 1; ABCL1; coronary heart disease;
KW dermatological; atherosclerosis; cardiovascular; inflammatory disease;
KW psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
KW immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 321..7106
FT /*tag= a
FT /product= "Human ABCL1 protein"
XX
EP1136552-Al.
XX
PD 26-SEP-2001.
XX
PF 20-MAR-2000; 2000EP-0105820.
XX
PR 20-MAR-2000; 2000EP-0105820.
XX
PA (FARB ) BAYER AG.
XX
PI Schmitz G, Bodzioch M;
XX
DR WPI: 2001-640389/74.
DR P-PSDB; AAE13022.
XX
PT New adenosine triphosphate binding cassette transporter-1 gene
PT polymorphisms, useful for diagnosing and treating lipid disorders,
PT cardiovascular diseases and inflammatory diseases
XX
PS Example 1; Fig 1; 48pp; English.
XX
CC The invention relates to four common polymorphisms in the gene encoding
CC ATP-binding cassette transporter-1 (ABCL1). ABCL1 is associated with
CC decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
CC ABCL1 directly affects cellular lipid homeostasis, which is a key factor
CC in the atherogenic processes. The ABCL1 polymorphisms are useful for
CC diagnosing and treating lipid disorders, cardiovascular diseases
CC (coronary heart disease, atherosclerosis) and inflammatory diseases
CC (psoriasis, lupus erythematosus). The identification of ABCL1 as a
CC transporter for interleukin-beta (IL-1beta) identifies this gene as
CC a candidate for treatment of inflammatory diseases including rheumatoid
CC arthritis and septic shock. The present sequence is human ABCL1 gene.
XX
SQ Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

Query Match 99.7%; Score 499.4; DB 22; Length 7260;
Best Local Similarity 99.8%; Pred. No. 2; le-136;
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGGCTGAAGAGACCATCGGGATC 60
DB 2280 GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGGCTGAAGAGACCATCGGGATC 2339
QY 61 ATGGSCCTGGACACAGCATACTCTGTTAGCTGGTTTCATTAGTACCTTCCTCTT 120
DB 2340 ATGGSCCTGGACACAGCATACTCTGTTAGCTGGTTTCATTAGTACCTTCCTCTT 2399
QY 121 CTGTGAGCGCTGGCGCTGCTAGTGGTCTATCTGAAAGTAGGAACCTGCTGCCCTACAGT 180
DB 2400 CTGTGAGCGCTGGCGCTGCTAGTGGTCTATCTGAAAGTAGGAACCTGCTGCCCTACAGT 2459
QY 181 GATCCACCGTGGTGTGTTGTTCTCTGCTCCGTGTTCTGCTGGTGACAACTTCGACGTGC 240

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DB 2460 GATCCACGCGTGGTGTGTTGTTCTTCTCTCCAGAGCCACCTGGCAGAGCTGTGGGGCATCATC 2519
QY 241 TTCCTGATTAGCACACTCTTCTCCAGAGCCACCTGGCAGAGCTGTGGGGCATCATC 300
DB 2520 TTCCTGATTAGCACACTCTTCTCCAGAGCCACCTGGCAGAGCTGTGGGGCATCATC 2579
QY 301 TACTTCACGCTGTACTGCCCTACGTCCTGTGTGTGGCATGCCAGGACTAGCTGGGCTTC 360
DB 2580 TACTTCACGCTGTACTGCCCTACGTCCTGTGTGTGGCATGCCAGGACTAGCTGGGCTTC 2639
QY 361 ACACATCAAGACTTTCGCTAGCCTGCTGCTCTCTGTTGGGTTTGGGTTTGGCTGTGAGTAC 420
DB 2640 ACACATCAAGACTTTCGCTAGCCTGCTGCTCTCTGTTGGGTTTGGGTTTGGCTGTGAGTAC 2699
QY 421 TTTGCCCTTTTGGAGGACGAGGCATTGGAGTGCAGTGGGACAACTGTTTGGAGAGTCCT 480
DB 2700 TTTGCCCTTTTGGAGGACGAGGCATTGGAGTGCAGTGGGACAACTGTTTGGAGAGTCCT 2759
QY 481 GTGGAGGAAGATGGCTCAAT 501
DB 2760 GTGGAGGAAGATGGCTCAAT 2780

RESULT 13
AAI70315
ID AAI70315 standard; cDNA; 7260 BP.
XX
AC AAI70315;
XX
DT 07-JAN-2002 (first entry)
XX
DE Human ATP binding cassette transporter 1 (ABCL1) cDNA.
XX
KW ATP binding cassette transporter 1; ABCL1; human; lipid disorder;
KW cholesterol; cardiovascular disease; inflammatory disease;
KW antinflammatory; antilipemic; antipsoriatic; dermatological;
KW Tangier disease; coronary heart disease; diagnosis; gene therapy;
KW polymorphism; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 321..7106
FT /*tag= a
FT CDS 501..7106
FT /*tag= b
FT variation /note= "alternative open reading frame of AAI70314"
FT /*tag= c
FT variation replace(1516,C)
FT /*tag= d
FT variation replace(2969,G)
FT /*tag= e
FT variation replace(3836,C)
FT /*tag= f
XX
EP1136554-Al.
XX
PD 26-SEP-2001.
XX
PF 24-MAR-2000; 2000EP-0106401.
XX
PR 24-MAR-2000; 2000EP-0106401.
XX
PA (FARB ) BAYER AG.
XX
PI Schmitz G, Bodzioch M;
XX
DR WPI: 2001-640389/74.
DR P-PSDB; AAM50228.
XX
PT New adenosine triphosphate binding cassette transporter gene

```

PT polymorphisms, useful for diagnosing and treating lipid disorders,  
PS cardiovascular diseases and inflammatory diseases  
XX Disclosure; Page 26-28; 41pp: English.

CC The present sequence is that of cDNA encoding the human adenosine  
CC triphosphate (ATP) binding cassette transporter 1 (ABCI1) protein  
CC (see AM50227). The sequence includes an extended open reading  
CC frame (ORF) to that provided by the sequence in AA170314, using  
CC an alternative ATG codon as initiation codon and thereby adding an  
CC extra 40 N-terminal amino acids to the encoded ABCI1 protein (see  
CC AM50228). The invention provides 4 common polymorphisms in the  
CC ABCI1 gene. These were identified by sequencing the ABCI1 gene in  
CC different Tangier kindreds. In the variant genes (numbering as in  
CC AA170314), G is changed to A at position 596. T is changed to C at  
CC position 1136, A is changed to G at position 2589 or G is changed  
CC to C at position 3456, or any combination of these. All of these  
CC polymorphisms alter the amino acid sequence of ABCI1 and therefore  
CC may affect its function. The 2 most common polymorphisms (G596A  
CC and A2589G) are both associated with a decreased in vitro ApoA-I  
CC mediated efflux of cholesterol from mononuclear phagocytes, a  
CC feature typical of Tangier disease. 3 Of the variants (G596A,  
CC A2589G and G3456C) are significantly increased in a population of  
CC men having low high density lipoprotein-cholesterol levels and  
CC established coronary heart disease (CHD) relative to CHD-free  
CC control subjects. The use of the provided ABCI1 polymorphisms for  
CC the diagnosis and treatment of lipid disorders, cardiovascular  
CC diseases, and inflammatory diseases (e.g. psoriasis, lupus  
CC erythematoses) is claimed. Modulation of ABCI1 transcripts or  
CC proteins by antisense or ribozyme technology or RNA decoys is also  
CC claimed.

XX Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;

|                       |   |                     |           |              |
|-----------------------|---|---------------------|-----------|--------------|
| Query Match           | 99.7%;  | Score 499.4;        | DB 22;    | Length 7260; |
| Best Local Similarity | 99.8%;  | Pred. No. 2.1e-136; |           |              |
| Matches 500;          | Conservative 0;   | Mismatches 1;       | Indels 0; | Gaps 0;      |
| QY 1                  | GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGCGCTGAAAGACCATCGCGATC   | 60                  |           |              |
| DB 2280               | GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGCGCTGAAAGACCATCGCGATC   | 2339                |           |              |
| QY 61                 | ATGGCCCTGGACACAGCATCTCTGTTAGCTGTTTACCTAGTACGCTCATTCCTCTT    | 120                 |           |              |
| DB 2340               | ATGGCCCTGGACACAGCATCTCTGTTTACCTAGTACGCTCATTCCTCTT           | 2399                |           |              |
| QY 121                | CTTGTGAGCGTGGCTGCTAGTGTCTATCTCTGAAAGTTAGGAACCTGCTGCCCTACAGT | 180                 |           |              |
| DB 2400               | CTTGTGAGCGTGGCTGCTAGTGTCTATCTCTGAAAGTTAGGAACCTGCTGCCCTACAGT | 2459                |           |              |
| QY 181                | GATCCAGCGTGGTGTGTTGCTTCCTGTCGCTGTTGCTGTGTTGCTGACATCTCGAGTGC | 240                 |           |              |
| DB 2460               | GATCCAGCGTGGTGTGTTGCTTCCTGTCGCTGTTGCTGTGTTGCTGACATCTCGAGTGC | 2519                |           |              |
| QY 241                | TTCTCTGATTAGCACACTCTCTCCAGAGCCAACTGGCAGCAGCTGTGGGGCATCATC   | 300                 |           |              |
| DB 2520               | TTCTCTGATTAGCACACTCTCTCCAGAGCCAACTGGCAGCAGCTGTGGGGCATCATC   | 2579                |           |              |
| QY 301                | TACTTCACGCTTACCTGCGCTTACCTGTTGTGTGTTGTTGTTGTTGTTGTTGTTGTTG  | 360                 |           |              |
| DB 2580               | TACTTCACGCTTACCTGCGCTTACCTGTTGTGTGTTGTTGTTGTTGTTGTTGTTG     | 2639                |           |              |
| QY 361                | ACATCAAGATCTTCGTAGCTGCTGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG  | 420                 |           |              |
| DB 2640               | ACATCAAGATCTTCGTAGCTGCTGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG  | 2699                |           |              |
| QY 421                | TTTGCCCTTTTTCAGGAGCAGGCGCATTTGGAGTGCAGTGGGACCACTGTTGAGAGTCT | 480                 |           |              |
| DB 2700               | TTTGCCCTTTTTCAGGAGCAGGCGCATTTGGAGTGCAGTGGGACCACTGTTGAGAGTCT | 2759                |           |              |
| QY 481                | GTGGAGGAAGATGGCTTCAAT                                       | 501                 |           |              |
| DB 2760               | GTGGAGGAAGATGGCTTCAAT                                       | 2780                |           |              |

RESULT 14  
AAK51683  
ID AAK51683 standard; cDNA; 7281 BP.

XX  
AC AAK51683;  
XX  
DT 06-NOV-2001 (first entry)

DE Human polynucleotide SEQ ID NO 228.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens.

PN WO200157190-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmarac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao OA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AZ, Yang Y, Wehrman T, Goodrich R;

XX WPI; 2001-476283/51.

DR P-PSDB; AAM78550.

XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -

XX Claim 1; Page 1086-1096; 6221pp: English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
CC (AAM80020) are omitted as the relevant pages from the sequence listing  
CC were missing at the time of publication.

XX Sequence 7281 BP; 1831 A; 1773 C; 1915 G; 1762 T; 0 other;

Query Match 99.7%; Score 499.4; DB 22; Length 7281;

Best Local Similarity 99.8%; Pred. No. 2.1e-136;

Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGCGCTGAAAGACCATCGCGATC 60

DB 2301 GTGATCATCAAGGGCATCGTGTATGAGAGGAGGACGCGCTGAAAGACCATCGCGATC 2360







Db 2336 TACTTCACGCTGTACCTGGCCCTACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTC 2395  
 QY 361 ACACICAAGATCTTCGCTAGCCTGCTGTCTCTCTGTGGCTTTGGGTTTGGCTGTGAGTAC 420  
 Db 2396 ACACICAAGATCTTCGCTAGCCTGCTGTCTCTCTGTGGCTTTGGGTTTGGCTGTGAGTAC 2455  
 QY 421 TTTGCCCTTTTTCAGGAGCAGGCGCATTTGGAGTCCAGTGGGACAACCTGTTGAGAGTCCT 480  
 Db 2456 TTTGCCCTTTTTCAGGAGCAGGCGCATTTGGAGTCCAGTGGGACAACCTGTTGAGAGTCCT 2515  
 QY 481 GTGGAGGAGATGGCTTCAAT 501  
 Db 2516 GTGGAGGAGATGGCTTCAAT 2536

Search completed: April 3, 2003, 13:36:30  
 Job time : 114.452 secs



GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.777 Seconds  
(without alignments)  
11152.306 Million cell updates/sec

Title: US-09-595-526C-1\_COPY\_2250\_2750

Perfect score: 501

Sequence: 1 gtgatacatcaaggccatcgt.....tggagggaagatggcttcaat 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

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4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.777 seconds  
(without alignments)  
11152.306 Million cell updates/sec

Title: US-09-595-526C-1\_COPY\_2250\_2750  
Perfect score: 501  
Sequence: 1 gtgatacatcaaggcatcgt.....tggaggaagatggcttcaat 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

US-08-665-259-24

Sequence 24, Application US/08665259

Patent No. 6028173

GENERAL INFORMATION:

APPLICANT: Landes, Gregory M.

APPLICANT: Burn, Timothy C.

APPLICANT: Connors, Timothy D.

APPLICANT: Dackowski, William R.

APPLICANT: Van Raay, Terence J.

APPLICANT: Klinger, Katherine W.

TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES.

TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENZYME CORPORATION

STREET: One Mountain Road

CITY: Framingham

STATE: Massachusetts

COUNTRY: United States of America

ZIP: 01701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,259

FILING DATE: 17-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dugan, Deborah A.

REGISTRATION NUMBER: 37,315

REFERENCE/DOCKET NUMBER: IG5-9.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508) 872-8400

TELEFAX: (508) 872-5415

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 5894 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 2..5053

US-08-665-259-24

Query Match 24.8% Score 124.2 DB 3 Length 5894

ALIGNMENTS

Sequence 21, Appl

Sequence 22, Appl

Sequence 2, Appl

Sequence 2, Appl

Sequence 31, Appl

Sequence 5, Appl

Sequence 5, Appl

Sequence 4, Appl

Sequence 4, Appl

Sequence 6, Appl

Sequence 6, Appl

Sequence 68, Appl

Sequence 11, Appl

Sequence 10, Appl

Sequence 1, Appl



|    | Query Match           | 24.88;  | Score 124.2;    | DB 3;      | Length 6525; |
|----|-----------------------|---|-----------------|------------|--------------|
|    | Best Local Similarity | 55.1%;  | Pred. No.       | 5.3e-29;   |              |
|    | Matches 274;          | Conservative 0;   | Mismatches 208; | Indels 15; | Gaps 17;     |
| QY | 17                    | TCGTGTTATGAAGAGGACGGCTGAAAGAGACCATCGGATCATGGCCCTGGACAACA          | 76              |            |              |
| Db | 1417                  | TCGTGCAGGAGAAGAAGGAGGCTGAGGAGTACATGCGCATGATGGGCTCAGCAGCT          | 1476            |            |              |
| QY | 77                    | GCATACTCTGGTTTAGCTGGTGTCATTAGTACGCCHCATPCCCTCTTTCTTGTAAGCCGCTGGCC | 136             |            |              |
| Db | 1477                  | GGCTGCACCTGGAGTGCCTGGTTCTCTTGTTCTTCCTCTTCCTCATCGCGGCTCCT          | 1536            |            |              |
| QY | 137                   | TGCTAGTGGTCACTCTGAAGTATA-----GGAAACCTGTCGCTACAGTG                 | 181             |            |              |
| Db | 1537                  | TCATGACCCTGCTCTCTGTGTCAAGGTGAAGCCAATGTAGCGTGTCTGCCACGG            | 1596            |            |              |
| QY | 182                   | ATCCAGCGTGGTGTTGTTCTTCCTGTCGCTGTTTTGCTGTGGTGACAACTCCCTGCAGTGC     | 241             |            |              |
| Db | 1597                  | ACCCCTCCCTGGTGTGCGCTTCCTGCTGCTGGCTCGCCATCTTACCATCTCCTTCAGCT       | 1656            |            |              |
| QY | 242                   | TCTGTATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCCTGTGGGGGCACTCAT       | 301             |            |              |
| Db | 1657                  | TCATGTCAGCACCTTCTTCAGAAAGCAACATGSCAGSAGCCCTTCGAGGCGTTCCTCT        | 1716            |            |              |
| QY | 302                   | ACTTCACGGTGTACCTGGCCCTAGCTCCTGTGTGGCATGGCAGGACTACGTGGGGCTCA       | 361             |            |              |
| Db | 1717                  | ACTTCTTACCTACATCCCTACTTCTTCTGGCGCCCCCTGGTACAACTGGATGATCTCTGA      | 1776            |            |              |

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Query Match      9.2%; Score 46; DB 1; Length 7218;
Best Local Similarity 5.6%; Pred No. 0.0022;
Matches 22; Conservative 206; Mismatches 166; Indels 0; Gaps 0;

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|    |      |   |      |
|----|------|---|------|
|    | 39   | GCTGAAGAGACCATCGGATCATCGGCCTGGACAACAGCATACTCTGGTTTACCTGGTT              | 98   |
| QY |      |   |      |
|    | 1017 | GCTCAGAGAATAATTCCGAGCTTGCTGCAGTCGAGGGAGCTTCGATYYYYYYYYYY                | 1076 |
| Db |      |   |      |
|    | 99   | CATTAGTAGCCCTCATCTCTCTGTGAGCGCTGGCTGCTACTGTGTCATCTCTGAAGTT              | 158  |
| QY |      | ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: |      |
|    | 1077 | YVVVYYYVV           | 1136 |
| Db |      |   |      |

```
QY 159 AGGAACCTGCTGCCCTACAGTATCCAGCGTGGTGTGTTCTCTCTCGTGTTCG 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1137 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1196

QY 219 TGTGGTACATCTGCACTGCTCTCTGATAGACACACTCTCTCCAGAGCAACTGGC 278
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1197 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1256

QY 279 AGCAGCTGTGGGGCATCTACTACCTGCTACCTGCTCCCTAGTCTCTGTGTGGC 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1257 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1316

QY 339 ATGCGAGTACTGGCTGCTACATCAGATCTTCGCTAGCTCTCTCTCTGGC 398
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1317 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1376

QY 399 TTTGGGTTGGCTGTGAGTACTTGGCCCTTTT 432
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1377 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1410

RESULT 5
US-09-295-593-37/c
; Sequence 37, Application US/09295593
; Patent No. 6417169
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: 032396-046
; CURRENT APPLICATION NUMBER: US/09/295,593
; CURRENT FILING DATE: 1999-04-22
; EARLIER APPLICATION NUMBER: US 60/082,791
; EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 37
; LENGTH: 4350
; TYPE: DNA
; ORGANISM: Human
US-09-295-593-37

Query Match 6.9%; Score 34.8; DB 4; Length 4350;
Best Local Similarity 58.8%; Pred. No. 0.55; Mismatches 42; Indels 0; Gaps 0;
Matches 60; Conservative 0;

QY 382 CTGCTGCTCTGCTGGCTTTGGTGTGGTGTGAGTACTTTGCCCTTTTTCAGGAGCAG 441
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1827 CTGTGTTCCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1768

QY 442 GGCATTGAGTGTGAGTGGGACACCTGTTTGAGAGTCCTGTG 483
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1767 TGTCTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1726

RESULT 6
US-09-149-476-284
; Sequence 284, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/043,312
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; EARLIER FILING DATE: 1997-04-11  
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 ; EARLIER FILING DATE: 1997-04-11  
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 ; EARLIER APPLICATION NUMBER: 60/049,610  
 ; EARLIER FILING DATE: 1997-06-13  
 ; EARLIER APPLICATION NUMBER: 60/061,060  
 ; EARLIER FILING DATE: 1997-10-02

Query Match 6.7% Score 33.4; DB 4; Length 961;

Best Local Similarity 46.6%; Pred. No. 0.68; Mismatches 117; Indels 0; Gaps 0; Matches 103; Conservative 1;

QY 270 CAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTACGCTGTACCTGCGCTACGCTCT 329  
 DB 490 CAACCTGGTGGGGCTCTGCGGCCCTGGCAGCATCTGGAGCGCGCGCGCATGCT 549  
 QY 330 GTGTGGCATGGCAGGACTACGTGGGCTTACACTCAAGATCTTCGCTAGCCGCTGTC 389  
 DB 550 GCGCTGTGTCTGTGGGGCTTTGCCCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 609  
 QY 390 TCCTGTGGCTTTTGGGTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGGAGGAGGAGG 449  
 DB 610 TCCCATCAGCAGCCCTCTTCCACACCCCACTTCTATGACAGGCTACAGGACGCGGCTCTCG 669  
 QY 450 AGTCAGTGGGACACCTGTTTGAGAGTCTCTGTGGAGAG 490  
 DB 670 CTGCCCCGAGCTTACCTCTATTCGAGGGCTGACGAGTAG 710

RESULT 7

US-09-634-920-3  
 ; Sequence 3, Application US/09634920  
 ; Patent No. 6342357  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Splawski, Igor  
 ; APPLICANT: Keating, Mark T.  
 ; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND  
 ; TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME

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; FILE REFERENCE: 2323-155
; CURRENT APPLICATION NUMBER: US/09/634,920
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/190,057
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6048)
US-09-634-920-3

Query Match      6.6%; Score 33; DB 4; Length 6048;
Best Local Similarity 53.5%; Pred. No. 2.4;
Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 133 GGCCTGCTAGTGGTCACTTGAAGTTAGGAACCTGCTGCCCTACAGTGTATCCACGCGG 192
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DB 2071 GCCAGCCTACCTGATCTGGAGTCTGCCCTGTGGATGCCATCAAGCAGGAGTG 2130

QY 193 GTGTTTGTCTTCCTGTCCTGCGTGGTGTGGTGACAACTCGCAGTGTCTCTGATTAC 252
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DB 2131 AAGTTGTGGTGGTCAAGCCGCTTACTGACCTCACCATCACTATGTGCATCTGACTCAAC 2190

QY 253 ACACCTCTTC 261
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DB 2191 ACACCTCTTC 2199

RESULT 8
US-09-149-476-145
; Sequence 145, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/056,877
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Query Match      6.5%; Score 32.8; DB 4; Length 1021;
Best Local Similarity 46.6%; Pred. No. 1.1; Mismatches 0; Gaps 0;
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Db 640 TCCATCAGACGCGCTTCCACCCACTTCTATGACAGGCTACAGGACGGGCTCTCG 699
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 450 AGTSCAGTGGACACACTGTTTGGAGAGTCTCTGTGGAGGAG 490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 700 CTGGCCGAGCTCTACTCTACTCGAGGCTGACGAAGTAG 740
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-280-116-109
; Sequence 109, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-109

Query Match      6.5%; Score 32.4; DB 4; Length 488;
Best Local Similarity 50.8%; Pred. No. 0.98; Mismatches 0; Gaps 0;
Matches 78; Conservative 0;

QY 212 TGTTTGTGTGGTGACAACTCTGCAGTGTCTCTGATAGACACTCTCTCCAGAGCCA 271
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 38 TGCTGACTGTGGCCACCGCCCTGATGTCGCCGTGAAGCCCCCGGGCTCTGGGGGCCCC 97
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 272 ACCTGGCAGCAGCCTGTGGGGGATCATCTACTTACGCTGTACCTGCCCTACGTCCTGT 331
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98 AGATCATCGGGGGCCAGGAGGTGACCCGCCACTCCAGGCCCTACATGCGTCGCTGCGCT 157
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 332 GTGTGGCATGCGAGGACTACGTGGGCTTCACACT 365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db  
158 TCGGGGGCCAAACATCATCTCGGAGGCTTCCTGCT 191

RESULT 10  
US-09-103-840A-2/C  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R. M  
; APPLICANT: FRASES, Eli M

APPLICANT: WENTER, John C.  
 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
 TITLE OF INVENTION: TUBERCULOSIS  
 FILE REFERENCE: 24366-20007.00  
 CURRENT APPLICATION NUMBER: US/09/103,840A  
 CURRENT FILING DATE: 1998-06-24  
 NUMBER OF SEQ ID NOS: 2  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2  
 LENGTH: 4403765  
 TYPE: DNA

```

ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      6.5%; Score 32.4; DB 4; Length 4403765;
Best Local Similarity 56.6%;
Matches 60; Conservative 0; Pred. No. 57;
Matches 46; Indels 0; Gaps 0;

```

| Accession | Gene | Strain  | Sequence   | Position |
|-----------|------|---------|--|----------|
| 344       | 2Y   | 403     | AGGACTACGTGGGCTTACACTCAAGATCTTCGTAGCCTGCTCTCTCTGTCGCTTGG | 403      |
| 4072293   | b    | 4072234 | AGGCAACGGCGCTCGACCCGAGTCTTCGATCTCCTCTTGTTCGAACGGGTTCTG   | 4072234  |
| 404       | 2Y   | 449     | GGTTTGCTGTGAGTACTTTGCCCTTTTGGAGGACAGGGCAATTGG            | 449      |
| 4072233   | b    | 4072188 | GGCTCGACTGGGGGAAGACCGACCTCGGAAGAGTTCACGGCGCTTG           | 4072188  |

RESULT 11  
S-09-103-840A-1/C  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.

APPLICANT: FRASER, Claire M.  
 APPLICANT: VENTER, John C.  
 TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TUBERCULOSIS  
 FILE REFERENCE: 24366-20007.00  
 CURRENT APPLICATION NUMBER: US/09/103,840A  
 CURRENT FILING DATE: 1998-05-24  
 NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
S-09-103-840A-1

```

Query Match          6.4%;      Score 32;  DB 4;  Length 441129;
Best Local Similarity 56.6%;      Pred. No. 62;
Matches 60;  Conservative 0;  Mismatches 46;  Indels 0;  Gaps 0;

344  AGGACTACGTGGGCTTCACATCAGATCTTCGTACGCTGCTCTCCGTGTGGCTTTTG 403
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
4080115  AGGGCAGCGGGCGGCTCGACCGGGAGTCTTCGATCTCTGTTGTCCGAACGGGTTTC
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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; SEQ ID NO 3
; LENGTH: 2912
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(2256)
US-09-307-143-3

Query Match      6.3%; Score 31.8; DB 4; Length 2912;
Best Local Similarity 49.1%; Pred. No. 3.9; Indels 0; Gaps 0;
Matches 84; Conservative 0; Mismatches 87;

QY 105 TAGCCTCATCTCTCTCTGTGAGCGCTGGCGCTAGTGGTGCATCCGGAAGTAGGAA 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 901 TAATCTTCTCTCTCTCTCTGTGCAACATCCTCTCTCTCTCTCTCTCTCTCTCT 842

QY 165 COTGTCGGCTACAGTATCCAGCGTGGTGTGTTCTCTCTCTCTCTCTCTCTCTCT 224
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 841 CATCTCAATTCAGGTTGTGCTCCGACTCTCTCTCTCTCTCTCTCTCTCTCTCT 782

QY 225 GACAATCCGTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 781 TGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 731

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RESULT 14
US-08-542-635-1/c
; Sequence 1, Application US/08542635
; Patent No. 6218356
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; APPLICANT: Letwin, Kenneth
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West, Box 401
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,635
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McDiarmid, Shona S.
; REGISTRATION NUMBER: 38,798
; REFERENCE/DOCKET NUMBER: 3153-162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; DEVELOPMENTAL STAGE: Embryo
; IMMEDIATE SOURCE:
; LIBRARY: lambda gt10 cDNA library

```

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; CLONE: Combined PHUKRACE A2 and K2 AND cDNA clones
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Distal end of chromosome 4
; MAP POSITION: near the ahd-1 mutation
US-08-542-635-1

Query Match      6.3%; Score 31.8; DB 4; Length 3105;
Best Local Similarity 48.1%; Pred. No. 4;
Matches 90; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 19 GTGTATGAGAAGGAGGACGCGCTGAAAGAGACCATCGGATCATGGCCCTGGACACAGC 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3060 GTGACAGACGACGAGGACCGACGTAGGGGCTCAGGGCGCGCTGGAGAGAGAGAAC 3001

QY 79 ATACTCTGGTTTACCTGGTTCAITAGTACCTCATTCCTCTCTCTCTCTCTCTCTCT 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3000 CGAGGCGAGCGGAATGTCACAACTCTACAGACTGGATCTGGTTCTATCTGGCCCCCATCAC 2941

QY 139 CTAGTGTGTCATCCCTGAAAGTTAGGAAAGCTGCTGCCCTACAGTATCCAGCGTGGTGT 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2940 CTGATACTGTTCAGGATTTTCTGTGGCCAGCTAGAGTGACCCCAACGCGGAGAAT 2881

QY 199 GTCCTCC 205
    ||| ||| |||
DB 2880 GTCCTCC 2874

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RESULT 15
US-08-318-905-21/c
; Sequence 21, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 117..1436  
US-08-318-905-21

Query Match 6.2%; Score 31.2; DB 1; Length 1494;  
Best Local Similarity 46.4%; Pred. No. 4.2;  
Matches 102; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

|    |      |  |      |
|----|------|--|------|
| Qy | 53   | TGCGGATCATGGCGCTGGACACAGCATACTCTGGTTTACCTGGTTCATTAGTAGCCTCA    | 112  |
| Db | 1408 | TGCTGAGCCGGGCGCTGGTGAAGGTTGACCTCAAGGGTGACCCAGGAATCAGGTTCTCATCA | 1349 |
| Qy | 113  | TTCCTCTTTGTGAGCGCTGCTAGTGGTCACTCCTGAAGTTAGGAAACCTGCTGC         | 172  |
| Db | 1348 | TCTCCTTCCACAGAGGGTCCCACTGATCAAAAGTCTTCTGAAGCCCTAAATGCTTTGT     | 1289 |
| Qy | 173  | CCTACAGTGAATCCAGCGTGGTTTGTCTTCTCTGTCGGTGTTCCTGTGGTGACAAATCC    | 232  |
| Db | 1288 | AAGAAAGCCATCGAAGCTTTGTTGGTGAAGTGGTACTGCTGGAATCGAATCTCTCT       | 1229 |
| Qy | 233  | TGCAGTGTCTTCCTGATTAGCACACTCTTCTCCAGAGCCAA                      | 272  |
| Db | 1228 | TTCAGTGTGAGCTGTGTTCCCAATTATTTGCCAGTTACAA                       | 1189 |

Search completed: April 3, 2003, 14:21:36  
Job time : 4321.78 secs

| Result No. | Score | Query |      | Length | DB                | ID | Description       |
|------------|-------|-------|------|--------|-------------------|----|-------------------|
|            |       | Match | %    |        |                   |    |                   |
| 1          | 501   | 100.0 | 9870 | 9      | US-09-984-827-101 |    | Sequence 101, App |
| 2          | 499.4 | 99.7  | 9825 | 9      | US-09-803-640-27  |    | Sequence 27, Appl |
| 3          | 499.4 | 99.7  | 9741 | 9      | US-09-984-827-1   |    | Sequence 1, Appl  |
| 4          | 499.4 | 99.7  | 9741 | 10     | US-09-846-456-10  |    | Sequence 10, Appl |
| 5          | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-92  |    | Sequence 92, Appl |
| 6          | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-93  |    | Sequence 93, Appl |
| 7          | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-94  |    | Sequence 94, Appl |
| 8          | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-95  |    | Sequence 95, Appl |
| 9          | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-96  |    | Sequence 96, Appl |
| 10         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-97  |    | Sequence 97, Appl |
| 11         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-98  |    | Sequence 98, Appl |
| 12         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-99  |    | Sequence 99, Appl |
| 13         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-100 |    | Sequence 100, App |
| 14         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-103 |    | Sequence 103, App |
| 15         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-104 |    | Sequence 104, App |
| 16         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-105 |    | Sequence 105, App |
| 17         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-106 |    | Sequence 106, App |
| 18         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-107 |    | Sequence 107, App |
| 19         | 499.4 | 99.7  | 9870 | 9      | US-09-984-827-108 |    | Sequence 108, App |

## SUMMARIES

| Query Match           | 99.7%          | Score 499.4  | DB 9     | Length 8925 |
|-----------------------|----------------|--|----------|-------------|
| Best Local Similarity | 99.8%          | Pred. No. 3,6e+154   |          |             |
| Matches 500           | Conservative 0 | Mismatches 1   | Indels 0 | Gaps 0      |
| QY                    | 1              | GTGATCATCAAGGGCATCGTATGAAGAGGACGCGCTGAAGAGACCATGGGATC        | 60       |             |
|                       |                |  |          |             |
| Db                    | 1899           | GTGATCATCAAGGGCATCGTATGAAGAGGACGCGCTGAAGAGACCATGGGATC        | 1958     |             |
|                       |                |  |          |             |
| QY                    | 61             | ATGGGCGCTGGACAACAGCATACTCTGGTTAGCTGGTTCATTAGTASCCTCATCTCTT   | 120      |             |
|                       |                |  |          |             |
| Db                    | 1959           | ATGGGCGCTGGACAACAGCATCTCTGTTTAGCTGGTTCATTAGTASCCTCATCTCTT    | 2018     |             |
|                       |                |  |          |             |
| QY                    | 121            | CTTGTGAGCGCTGGCGCTGCTAGTGGTTCATCTGAAGTTAGGAACCTGCTGCCCTACAGT | 180      |             |
|                       |                |  |          |             |
| Db                    | 2019           | CTTGTGAGCGCTGGCGCTGCTAGTGGTTCATCTGAAGTTAGGAACCTGCTGCCCTACAGT | 2078     |             |
|                       |                |  |          |             |
| QY                    | 181            | GATCCACAGCGTGGTGTGTTGTCCTCTCGCTGTTTGGTCTGTGTGACAACTCTGCAGTC  | 240      |             |

|    | Query Match           | 99.7%   | Score        | 499.4;        | DB         | 9; | Length | 9741; |
|----|-----------------------|---|--------------|---------------|------------|----|--------|-------|
|    | Best Local Similarity | 99.8%;  | Pred.        | No. 3.7e-154; |            |    |        |       |
|    | Matches               | 500;  | Conservative | 0;            | Mismatches | 1; | Indels | 0;    |
|    |                       |   |              |               |            |    |        | Gaps  |
| QY | 1                     | GTGATCATCAAGGCGATCGTGTATGAGAAGGAGGACGGGTGAAAGAGACCATCGCGATC       | 60           |               |            |    |        |       |
| Db | 2144                  | GTGATCATCAAGGCGATCGTGTATGAGAAGGAGGACGGGTGAAAGAGACCATCGCGATC       | 2203         |               |            |    |        |       |
| QY | 61                    | ATSGGCGCTGGACAAACAGCATACTCTGTGTTTACGTGGTTCATTAGTAGCCGCATCTCCCTTT  | 120          |               |            |    |        |       |
| Db | 2204                  | ATGGGCGCTGGACAAACAGCATCTCTGTGTTTACGTGGTTCATTAGTAGCCGCATCTCCCTTT   | 2263         |               |            |    |        |       |
| QY | 121                   | CTTGTGAGCGCTGGCGCTGCTAGTGTGTCATCTGAAGTAGAGAAACCTGCCTGCCTACAGT     | 180          |               |            |    |        |       |
| Db | 2264                  | CTTGTGAGCGCTGGCGCTGCTAGTGTGTCATCTGAAGTAGAGAAACCTGCCTGCCTACAGT     | 2323         |               |            |    |        |       |
| QY | 181                   | GATCCCGACGGTGGTGTGTTTGCTTCTCTGTCCTGTGTTGCTGTGGTGCACAATCCCTGCAGTGC | 240          |               |            |    |        |       |

|    |      |  |      |
|----|------|--|------|
| Db | 2324 | GATCCACGGTGTGTTTGTTCTTCCTGTCGCGTGTTCGTGTGGTGAACAATCCTGCAGTGC   | 2383 |
| QY | 241  | TTCTCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGACAGCCTGTGGGGCATCATC  | 300  |
| Db | 2384 | TTCCTGATTAGCACACTCTTCTCCAGAGCCAACCTGGCAGACAGCCTGTGGGGCATCATC   | 2443 |
| QY | 301  | TACTTCACCTGTACCTGCCCTACGTCCTGTGTGTGTGGCATGGCAGAGCACTAGTGGGGTTC | 360  |
| Db | 2444 | TACTTCACCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGAGCACTAGTGGGGTTC   | 2503 |
| QY | 361  | ACACTCAAGATCTTCGCTAGCCTGCTGTCCTCTGTGGCTTTTGGGTTTGCGTGTGAGTAC   | 420  |
| Db | 2504 | ACACTCAAGATCTTCGCTAGCCTGCTGTCCTCTGTGGCTTTTGGGTTTGCGTGTGAGTAC   | 2563 |
| QY | 421  | TTTGCCCTTTTTCAGAGCAGGGCATGGAGTGCAGTGGGACAACCTGTTTTCAGAGTCCT    | 480  |
| Db | 2564 | TTTGCCCTTTTTCAGAGCAGGGCATGGAGTGCAGTGGGACAACCTGTTTTCAGAGTCCT    | 2623 |
| QY | 481  | GTGGAGGAAGATGGCTTCAAT  | 501  |
| Db | 2624 | GTGGAGGAAGATGGCTTCAAT  | 2644 |

```

RESULT 4
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Denefle, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Renaley, Alan
; APPLICANT: Pojo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

```

|    | Query Match           | 99.7%   | Score 499.4        | DB 10  | Length 9741 |
|----|-----------------------|---|--------------------|--------|-------------|
|    | Best Local Similarity | 99.8%   | Pred. No. 3.7e-154 | Indels | 0           |
|    | Matches 500           | Conservative 0  | Mismatches 1       | Gaps   | 0           |
| Qy | 1                     | GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGACGGCTGAAAGACCATGCGGATC   | 60                 |        |             |
|    |                       |   |                    |        |             |
| Db | 2144                  | GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGACGGCTGAAAGACCATGCGGATC   | 2203               |        |             |
|    |                       |   |                    |        |             |
| Qy | 61                    | ATGGCCCTGGACACAGCATCTCGTTTACGTGGTTCATTAGTAGCCTCATTCCTCTT    | 120                |        |             |
|    |                       |   |                    |        |             |
| Db | 2204                  | ATGGCCCTGGACACAGCATCTCGTTTACGTGGTTCATTAGTAGCCTCATTCCTCTT    | 2263               |        |             |
|    |                       |   |                    |        |             |
| Qy | 121                   | CTTGTGAGCGTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT | 180                |        |             |
|    |                       |   |                    |        |             |
| Db | 2264                  | CTTGTGAGCGTGGCCTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT | 2323               |        |             |
|    |                       |   |                    |        |             |
| Qy | 181                   | GATCCACGCTGCTTTTGTCTTCCTGTCGGTGTGTTGTGTGGTCACAACTCTGCAGTGC  | 240                |        |             |

|    |      |  |      |
|----|------|--|------|
| Db | 2324 | GATCCAGCGTGGTGTTCCTTCCTGTCCTCGTGTTGGTCGTGAGCAATCCTCGACATGC     | 2383 |
| Qy | 241  | TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGACGCTGTGGGGGCATCATC      | 300  |
| Db | 2384 | TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGACGCTGTGGGGGCATCATC      | 2443 |
| Qy | 301  | TACTTCACGCTGTACCTTGGCTTACGTCCTCTGCTGTGGCATGGCAGGACTAGCTGGGCTTC | 360  |
| Db | 2444 | TACTTCACGCTGTACCTTGGCTTACGTCCTCTGCTGTGGCATGGCAGGACTAGCTGGGCTTC | 2503 |
| Qy | 361  | ACACTCAAGATCTTCCTAGCTGCTGTCTCCTCTGGGCTTTTGGGTTTGGCTGTGAGTAC    | 420  |
| Db | 2504 | ACACTCAAGATCTTCCTAGCTGCTGTCTCCTCTGGGCTTTTGGGTTTGGCTGTGAGTAC    | 2563 |
| Qy | 421  | TTTGCCCTTTTTCAGGAGCAGGSCATTTGGAGTCAGTCGGGACAACTCTTTTGAGAGTCCT  | 480  |
| Db | 2564 | TTTGCCCTTTTTCAGGAGCAGGSCATTTGGAGTCAGTCGGGACAACTCTTTTGAGAGTCCT  | 2623 |
| Qy | 481  | GTGGAGGAAGATGCTTCAAT   | 501  |
| Db | 2624 | GTGGAGGAAGATGCTTCAAT   | 2644 |

RESULT 5  
 US-09-984-827-92  
 ; Sequence 92, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFFE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR  
 ; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984,827  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn ver. 2.1  
 ; SEQ ID NO 92  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 HS-09-984-827-92

| Query Match           | 99.7%        | Score 499.4   | DB 9         | Length 9870 |        |
|-----------------------|--------------|---|--------------|-------------|--------|
| Best Local Similarity | 99.8%        | Pred. No. 3.8e-154  |              |             |        |
| Matches 500           | Conservative | 0   | Mismatches 1 | Indels 0    | Gaps 0 |
| QY                    | 1            | GTGATCATCAAGGGCATCGTGATGAGGAAGGAGGCACGGCTGAAAGAGACCATCGGGATC    | 60           |             |        |
| Db                    | 2273         | GTGATCATCAAGGGCATCGTGATGAGGAAGGAGGCACGGCTGAAAGAGACCATCGGGATC    | 2332         |             |        |
| QY                    | 61           | ATGGGCGCTGGACAACAGCATACTCGTGTATAGCTGGTTCATTAGTAGCTCATCTCCTCTT   | 120          |             |        |
| Db                    | 2333         | ATGGGCGCTGGACAACAGCATACTCGTGTATAGCTGGTTCATTAGTAGCTCATCTCCTCTT   | 2392         |             |        |
| QY                    | 121          | CTTTGTGAGGCGTGGCGTGTCTATGTGTGCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT | 180          |             |        |
| Db                    | 2393         | CTTTGTGAGGCGTGGCGTGTCTATGTGTGCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGT | 2452         |             |        |
| QY                    | 181          | GATCCAGCGTGGTGTTTGTCTTTCCTGTGTCCTGTGTTTGTGTGGTGACAAATCTGCAGTGC  | 240          |             |        |
| Db                    | 2453         | GATCCAGCGTGGTGTTTGTCTTTCCTGTGTCCTGTGTTTGTGTGGTGACAAATCTGCAGTGC  | 2512         |             |        |





Db 2513 TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGACGCTGTGGGGGCATCATC 2572  
QY 301 TACTTACAGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360  
Db 2573 TACTTACAGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632  
QY 361 ACACCTAAGATCTTCGCTAGCCTGTCTCCCTGTGGCTTTTGGCTGTGAGTAC 420  
Db 2633 ACACCTAAGATCTTCGCTAGCCTGTCTCCCTGTGGCTTTTGGCTGTGAGTAC 2692  
QY 421 TTGGCCCTTTTGGAGGAGGAGGATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 480  
Db 2693 TTGGCCCTTTTGGAGGAGGAGGATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 2752  
QY 481 GTGAGGAAGATGGCTTCAAT 501  
Db 2753 GTGAGGAAGATGGCTTCAAT 2773

## RESULT 8

US-09-984-827-95  
; Sequence 95, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEUFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARMOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-95

Query Match 99.7%; Score 499.4; DB 9; Length 9870;  
Best Local Similarity 99.8%; Pred. No. 3.8e-154;  
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GTGATCATCAAGGCACTCTGTATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATC 60  
Db 2273 GTGATCATCAAGGCACTCTGTATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATC 2332  
QY 61 ATGGGCTGGACAAACAGCATCTCTGTTAGCTGTGTTTCAATTAGTACGCTTCATTCCTCTT 120  
Db 2333 ATGGGCTGGACAAACAGCATCTCTGTTAGCTGTGTTTCAATTAGTACGCTTCATTCCTCTT 2392  
QY 121 CTGTGAGCGCTGGCCCTGTAGTGGTCATCCTGGAAGTATAGAAACCTGTGCCCTACAGT 180  
Db 2393 CTGTGAGCGCTGGCCCTGTAGTGGTCATCCTGGAAGTATAGAAACCTGTGCCCTACAGT 2452  
QY 181 GATCCAGCGTGGTGTTCCTCTCGTCTGTTTCTGTTGAGCAACCTGCGAGTGC 240  
Db 2453 GATCCAGCGTGGTGTTCCTCTCGTCTGTTTCTGTTGAGCAACCTGCGAGTGC 2512  
QY 241 TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300  
Db 2513 TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

Db 2513 TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572  
QY 301 TACTTACAGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 360  
Db 2573 TACTTACAGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632  
QY 361 ACACCTAAGATCTTCGCTAGCCTGTCTCCCTGTGGCTTTTGGCTGTGAGTAC 420  
Db 2633 ACACCTAAGATCTTCGCTAGCCTGTCTCCCTGTGGCTTTTGGCTGTGAGTAC 2692  
QY 421 TTGGCCCTTTTGGAGGAGGAGGATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 480  
Db 2693 TTGGCCCTTTTGGAGGAGGAGGATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 2752  
QY 481 GTGAGGAAGATGGCTTCAAT 501  
Db 2753 GTGAGGAAGATGGCTTCAAT 2773

## RESULT 9

US-09-984-827-96  
; Sequence 96, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEUFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARMOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 96  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-96

Query Match 99.7%; Score 499.4; DB 9; Length 9870;  
Best Local Similarity 99.8%; Pred. No. 3.8e-154;  
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GTGATCATCAAGGCACTCTGTATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATC 60  
Db 2273 GTGATCATCAAGGCACTCTGTATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATC 2332  
QY 61 ATGGGCTGGACAAACAGCATCTCTGTTAGCTGTGTTTCAATTAGTACGCTTCATTCCTCTT 120  
Db 2333 ATGGGCTGGACAAACAGCATCTCTGTTAGCTGTGTTTCAATTAGTACGCTTCATTCCTCTT 2392  
QY 121 CTGTGAGCGCTGGCCCTGTAGTGGTCATCCTGGAAGTATAGAAACCTGTGCCCTACAGT 180  
Db 2393 CTGTGAGCGCTGGCCCTGTAGTGGTCATCCTGGAAGTATAGAAACCTGTGCCCTACAGT 2452  
QY 181 GATCCAGCGTGGTGTTCCTCTCGTCTGTTTCTGTTGAGCAACCTGCGAGTGC 240  
Db 2453 GATCCAGCGTGGTGTTCCTCTCGTCTGTTTCTGTTGAGCAACCTGCGAGTGC 2512  
QY 241 TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGCAGCCTGTGGGGGCATCATC 300  
Db 2513 TTCTGATTAGCACACTCTTCTCCAGAGCAACCTGGCAGCAGCCTGTGGGGGCATCATC 2572

QY 301 TACTTACCGCTGTACCTGCCCTACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTC 360  
 Db 2573 TACTTACCGCTGTACCTGCCCTACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632  
 QY 361 ACACCTCAAGATCTTCCTAGCTGCTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420  
 Db 2633 ACACCTCAAGATCTTCCTAGCTGCTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692  
 QY 421 TTGGCCCTTTTGGAGGAGGAGCAATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 480  
 Db 2693 TTGGCCCTTTTGGAGGAGGAGCAATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 2752  
 QY 481 GTGGAGGAAGATGGCTCAAT 501  
 Db 2753 GTGGAGGAAGATGGCTTCAAT 2773

RESULT 10  
 US-09-984-827-97  
 ; Sequence 97, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFFLE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984,827  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 97  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-97

Query Match 99.7%; Score 499.4; DB 9; Length 9870;  
 Best Local Similarity 99.8%; Pred. No. 3.8e-154;  
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGACGCGCTGAAAGAGACCATCGCGATC 60  
 Db 2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGACGCGCTGAAAGAGACCATCGCGATC 2332  
 QY 61 ATGGGCTGGACACAGCATCTGTTAGCTGGTTTCAATTAGTAGCCTCATTCCTCTT 120  
 Db 2333 ATGGGCTGGACACAGCATCTGTTAGCTGGTTTCAATTAGTAGCCTCATTCCTCTT 2392  
 QY 121 CTGTGAGCGCTGGCTGTAGTGGTTCATCTGAAAGTAGGAAACCTGCTGCCCTACAGT 180  
 Db 2393 CTGTGAGCGCTGGCTGTAGTGGTTCATCTGAAAGTAGGAAACCTGCTGCCCTACAGT 2452  
 QY 181 GATCCAGCGTGGTGTTCCTGTCCTGCTGTTTCTGCTGGTGAACAATCCTGCGAGTGC 240  
 Db 2453 GATCCAGCGTGGTGTTCCTGTCCTGCTGTTTCTGCTGGTGAACAATCCTGCGAGTGC 2512  
 QY 241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATC 300  
 Db 2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATC 2572

QY 301 TACTTACCGCTGTACCTGCCCTACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTC 360  
 Db 2573 TACTTACCGCTGTACCTGCCCTACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632  
 QY 361 ACACCTCAAGATCTTCCTAGCTGCTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 420  
 Db 2633 ACACCTCAAGATCTTCCTAGCTGCTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTAC 2692  
 QY 421 TTGGCCCTTTTGGAGGAGGAGCAATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 480  
 Db 2693 TTGGCCCTTTTGGAGGAGGAGCAATGGAGTGCAGTGGGACAACTGTTTGGAGAGTCT 2752  
 QY 481 GTGGAGGAAGATGGCTCAAT 501  
 Db 2753 GTGGAGGAAGATGGCTTCAAT 2773

RESULT 11  
 US-09-984-827-98  
 ; Sequence 98, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFFLE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984,827  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 98  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-98

Query Match 99.7%; Score 499.4; DB 9; Length 9870;  
 Best Local Similarity 99.8%; Pred. No. 3.8e-154;  
 Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGACGCGCTGAAAGAGACCATCGCGATC 60  
 Db 2273 GTGATCATCAAGGGCATCGTGTATGAGAAGGAGGACGCGCTGAAAGAGACCATCGCGATC 2332  
 QY 61 ATGGGCTGGACACAGCATCTGTTAGCTGGTTTCAATTAGTAGCCTCATTCCTCTT 120  
 Db 2333 ATGGGCTGGACACAGCATCTGTTAGCTGGTTTCAATTAGTAGCCTCATTCCTCTT 2392  
 QY 121 CTGTGAGCGCTGGCTGTAGTGGTTCATCTGAAAGTAGGAAACCTGCTGCCCTACAGT 180  
 Db 2393 CTGTGAGCGCTGGCTGTAGTGGTTCATCTGAAAGTAGGAAACCTGCTGCCCTACAGT 2452  
 QY 181 GATCCAGCGTGGTGTTCCTGTCCTGCTGTTTCTGCTGGTGAACAATCCTGCGAGTGC 240  
 Db 2453 GATCCAGCGTGGTGTTCCTGTCCTGCTGTTTCTGCTGGTGAACAATCCTGCGAGTGC 2512  
 QY 241 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATC 300  
 Db 2513 TTCCTGATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATC 2572  
 QY 301 TACTTACCGCTGTACCTGCCCTACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTC 360

Db 2573 TACTTCAAGCTGTACCTGCGCTACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632  
QY 361 ACACCTCAAGATCTTCGTAGCCTGCTGTCTCTCTGTGGCTTTTGGCTGTAGTAC 420  
Db 2633 ACACCTCAAGATCTTCGTAGCCTGCTGTCTCTCTGTGGCTTTTGGCTGTAGTAC 2692  
QY 421 TTTGGCCCTTTTGGAGGAGGCGCATTTGGAGTGCAGTGGGACCAACCTGTTGAGAGTCTC 480  
Db 2693 TTTGGCCCTTTTGGAGGAGGCGCATTTGGAGTGCAGTGGGACCAACCTGTTGAGAGTCTC 2752  
QY 481 GTGGAGGAGATGCTTCAAT 501  
Db 2753 GTGGAGGAGATGCTTCAAT 2773

## RESULT 12

US-09-984-827-99  
; Sequence 99, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984, 827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 99  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-99

Query Match 99.7%; Score 499.4; DB 9; Length 9870;  
Best Local Similarity 99.8%; Pred. No. 3.8e-154;  
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCATCAAGGCGATCGTGTATGAGAGGAGGCGCGCTGAAAGAGACCATCGCGATC 60  
Db 2273 GTGATCATCAAGGCGATCGTGTATGAGAGGAGGCGCGCTGAAAGAGACCATCGCGATC 2332  
QY 61 ATGGGCGCTGGACAAACAGCATCTCTGTTTGTAGTGTGTTTGTATTAGTACGCTTCCTCTT 120  
Db 2333 ATGGGCGCTGGACAAACAGCATCTCTGTTTGTAGTGTGTTTGTATTAGTACGCTTCCTCTT 2392  
QY 121 CTGTGTAGGCGCTGGCGCTGTAGTGTCTATCCTGAAAGTGGGAAACCTGTCGCCCTACAGT 180  
Db 2393 CTGTGTAGGCGCTGGCGCTGTAGTGTCTATCCTGAAAGTGGGAAACCTGTCGCCCTACAGT 2452  
QY 181 GATCCAGCGCTGGTGTGTTTGTCTTCCTGTCGCTGTTTGTCTGTGTGACATCTCGCAGTGC 240  
Db 2453 GATCCAGCGCTGGTGTGTTTGTCTTCCTGTCGCTGTTTGTCTGTGTGACATCTCGCAGTGC 2512  
QY 241 TTCTGTATTAGCACACTCTTCTCCAGAGCCAACTTCCAGAGCCGCTGTGGGGGCATCATC 300  
Db 2513 TTCTGTATTAGCACACTCTTCTCCAGAGCCAACTTCCAGAGCCGCTGTGGGGGCATCATC 2572  
QY 301 TACTTCAAGCTGTACCTGCGCTACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTC 360

Db 2573 TACTTCAAGCTGTACCTGCGCTACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632  
QY 361 ACACCTCAAGATCTTCGTAGCCTGCTGTCTCTCTGTGGCTTTTGGCTGTAGTAC 420  
Db 2633 ACACCTCAAGATCTTCGTAGCCTGCTGTCTCTCTGTGGCTTTTGGCTGTAGTAC 2692  
QY 421 TTTGGCCCTTTTGGAGGAGGCGCATTTGGAGTGCAGTGGGACCAACCTGTTGAGAGTCTC 480  
Db 2693 TTTGGCCCTTTTGGAGGAGGCGCATTTGGAGTGCAGTGGGACCAACCTGTTGAGAGTCTC 2752  
QY 481 GTGGAGGAGATGCTTCAAT 501  
Db 2753 GTGGAGGAGATGCTTCAAT 2773

## RESULT 13

US-09-984-827-100  
; Sequence 100, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984, 827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-100

Query Match 99.7%; Score 499.4; DB 9; Length 9870;  
Best Local Similarity 99.8%; Pred. No. 3.8e-154;  
Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCATCAAGGCGATCGTGTATGAGAGGAGGCGCGCTGAAAGAGACCATCGCGATC 60  
Db 2273 GTGATCATCAAGGCGATCGTGTATGAGAGGAGGCGCGCTGAAAGAGACCATCGCGATC 2332  
QY 61 ATGGGCGCTGGACAAACAGCATCTCTGTTTGTAGTGTGTTTGTATTAGTACGCTTCCTCTT 120  
Db 2333 ATGGGCGCTGGACAAACAGCATCTCTGTTTGTAGTGTGTTTGTATTAGTACGCTTCCTCTT 2392  
QY 121 CTGTGTAGGCGCTGGCGCTGTAGTGTCTATCCTGAAAGTGGGAAACCTGTCGCCCTACAGT 180  
Db 2393 CTGTGTAGGCGCTGGCGCTGTAGTGTCTATCCTGAAAGTGGGAAACCTGTCGCCCTACAGT 2452  
QY 181 GATCCAGCGCTGGTGTGTTTGTCTTCCTGTCGCTGTTTGTCTGTGTGACATCTCGCAGTGC 240  
Db 2453 GATCCAGCGCTGGTGTGTTTGTCTTCCTGTCGCTGTTTGTCTGTGTGACATCTCGCAGTGC 2512  
QY 241 TTCTGTATTAGCACACTCTTCTCCAGAGCCAACTTCCAGAGCCGCTGTGGGGGCATCATC 300  
Db 2513 TTCTGTATTAGCACACTCTTCTCCAGAGCCAACTTCCAGAGCCGCTGTGGGGGCATCATC 2572  
QY 301 TACTTCAAGCTGTACCTGCGCTACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTC 360  
Db 2573 TACTTCAAGCTGTACCTGCGCTACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTC 2632



Db 2633 ACCTCAAGATCTTGGCTAGCTGCTGCTCCTGCTGGCTTTTGGGTTGGCTGTGAGTAC 2692  
Qy 421 TTGCCCCCTTTTGAGGAGCAGGCGCATTTGGAGTGCAGTGGGACACCTGTTTGAGAGTCCT 480  
Db 2693 TTGCCCCCTTTTGAGGAGCAGGCGCATTTGGAGTGCAGTGGGACACCTGTTTGAGAGTCCT 2752  
Qy 481 GTGGAGGAGATGGCTTCAAT 501  
Db 2753 GTGGAGGAGATGGCTTCAAT 2773

Search completed: April 4, 2003, 06:41:55  
Job time : 64.6923 secs



|   |   |
|---|---|
| OM nucleic - nucleic search, using sw model                 |   |
| Run on:   | April 3, 2003, 09:40:44 ; Search time 566.323 Seconds<br>(without alignments)<br>14327.411 Million cell updates/sec |
| Title: US-09-595-526c-1_COPY_2250_2750                      |   |
| Perfect score:  | 501   |
| Sequence:   | 1 gtgatcatcaaggcatcgt.....tggagggaagatggcttcaat 501   |
| Scoring table: IDENTITY_NUC                                 |   |
| Gapop 10.0 , Gapext 1.0                                     |   |
| Searched: 16154066 seqs, 8097743376 residues                |   |
| Total number of hits satisfying chosen parameters: 32308132 |   |
| Minimum DB seq length: 0                                    |   |
| Maximum DB seq length: 2000000000                           |   |
| Post-processing: Minimum Match 0%                           |   |
| Maximum Match 100%  |   |
| Listing first 45 summaries                                  |   |
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| 1: em_estba:*   |   |
| 2: em_esthum:*  |   |
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| 8: em_hic:*   |   |
| 9: gb_esti:*  |   |
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| 19: em_gss_inv:*  |   |
| 20: em_gss_pln:*  |   |
| 21: em_gss_vit:*  |   |
| 22: em_gss_fun:*  |   |
| 23: em_gss_mam:*  |   |
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| 25: em_gss_other:*  |   |
| 26: em_gss_pro:*  |   |
| 27: em_gss_rod:*  |   |

|    |       |      |      |    |           |
|----|-------|------|------|----|-----------|
| 7  | 186   | 37.1 | 2640 | 11 | U66691    |
| 8  | 164.2 | 31.8 | 850  | 14 | W29003    |
| 9  | 156.4 | 31.2 | 833  | 17 | CNS032BC  |
| 10 | 142   | 28.3 | 1119 | 17 | CNS035SG  |
| 11 | 120.4 | 24.0 | 670  | 17 | AZ721290  |
| 12 | 101   | 20.2 | 375  | 12 | BF928780  |
| 13 | 96.4  | 19.2 | 969  | 17 | CNS032VK  |
| 14 | 93.6  | 18.7 | 732  | 12 | BF08713   |
| 15 | 91.8  | 18.3 | 408  | 9  | AA772600  |
| 16 | 90.2  | 18.0 | 476  | 12 | BF16223   |
| 17 | 89    | 17.8 | 475  | 14 | BQ346986  |
| 18 | 85.6  | 17.1 | 1009 | 17 | CNS03EYX  |
| 19 | 83    | 16.6 | 986  | 14 | BQ921813  |
| 20 | 82    | 16.4 | 950  | 17 | CNS042PO  |
| 21 | 79    | 15.8 | 672  | 17 | BH260053  |
| 22 | 77.4  | 15.4 | 956  | 17 | CNS03OKO  |
| 23 | 76.8  | 15.3 | 564  | 17 | FR0029378 |
| 24 | 75.2  | 15.0 | 379  | 9  | AI050892  |
| 25 | 74.6  | 14.9 | 191  | 13 | BI039809  |
| 26 | 72.6  | 14.5 | 210  | 17 | CNS03ZVJ  |
| 27 | 71.6  | 14.3 | 1032 | 13 | BI659235  |
| 28 | 69.8  | 13.9 | 729  | 13 | BI330649  |
| 29 | 65    | 13.0 | 404  | 12 | BG152462  |
| 30 | 63.8  | 12.7 | 317  | 12 | BF922869  |
| 31 | 63.8  | 12.7 | 831  | 17 | AQ747504  |
| 32 | 63.6  | 12.7 | 999  | 17 | CNS03IS9  |
| 33 | 62.2  | 12.4 | 825  | 17 | CNS04KMC  |
| 34 | 61.4  | 12.3 | 913  | 17 | CNS03NGC  |
| 35 | 61.4  | 12.3 | 925  | 17 | CNS04IM7  |
| 36 | 58.6  | 11.7 | 1093 | 17 | CNS02AFG  |
| 37 | 58.4  | 11.7 | 1107 | 14 | BQ708777  |
| 38 | 57.4  | 11.5 | 589  | 17 | FR0029372 |
| 39 | 56.2  | 11.2 | 878  | 17 | CNS05SPE  |
| 40 | 56.2  | 11.2 | 1003 | 17 | CNS03SE9  |
| 41 | 56    | 11.2 | 1087 | 17 | CNS0556V  |
| 42 | 54.4  | 10.9 | 340  | 17 | AZ305988  |
| 43 | 52.6  | 10.5 | 487  | 17 | AQ846043  |
| 44 | 51.8  | 10.3 | 349  | 14 | BQ344563  |
| 45 | 51    | 10.2 | 571  | 12 | BF189018  |

ALIGNMENTS

|            |   |              |                |                  |                 |
|------------|---|--------------|----------------|------------------|-----------------|
| RESULT 1   | BI754756  | 809 bp       | mRNA           | linear           | EST 25-SEP-2001 |
| BI754756   | 603025477F1 NIH_MGC_114   | Homo sapiens | CDNA clone     | IMAGE:5195995 5' |                 |
| LOCUS      | BI754756  |              | mRNA sequence. |                  |                 |
| DEFINITION | BI754756.1  | GI:15746334  |                |                  |                 |
| ACCESSION  | BI754756  |              |                |                  |                 |
| VERSION    | EST.  |              |                |                  |                 |
| KEYWORDS   | Human.  |              |                |                  |                 |
| SOURCE     | Human.  |              |                |                  |                 |
| ORGANISM   | Homo sapiens  |              |                |                  |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |              |                |                  |                 |
| AUTHORS    | NIH-MGC http://mgc.nci.nih.gov/   |              |                |                  |                 |
| TITLE      | National Institutes of Health, Mammalian Gene Collection (MGC)  |              |                |                  |                 |
| JOURNAL    | Unpublished (1999)  |              |                |                  |                 |
| COMMENT    | Contact: Robert Strausberg, Ph.D.<br>Email: cgabbs@mail.nih.gov<br>Tissue Procurement: Life Technologies, Inc.<br>CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)<br>DNA Sequencing by: Incyte Genomics, Inc.<br>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov<br>Plate: LLAM11490 row: i column: 20<br>High quality sequence stop: 768.<br>Location/Qualifiers<br>1..809 |              |                |                  |                 |

FEATURES  
source

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 490   | 97.8        | 809    | 13 | BI754756 603025477 |
| 2          | 285.8 | 57.0        | 324    | 10 | AW845151 RC0-CT000 |
| 3          | 242   | 48.3        | 333    | 9  | AI344681 qp09h03.x |
| 4          | 228.8 | 45.7        | 491    | 12 | BF979888 RC2-ET018 |
| 5          | 205.4 | 41.0        | 427    | 13 | BM153383 TCBA2D11  |
| 6          | 196.6 | 39.2        | 351    | 12 | BF928185 CM4-NT021 |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





| ORGANISM  | TITLE   |
|---|---|
| <p>Homo sapiens<br/>Eumkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br/>Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.<br/>1 (bases 1 to 491)</p> | <p>Shotgun sequencing of the human transcriptome with ORF expressed<br/>sequence tags<br/>Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)</p>  |
| <p>REFERENCE<br/>AUTHORS</p>  | <p>20202663<br/>Contact: Simpson A.J.G.<br/>Laboratory of Cancer Genetics<br/>Ludwig Institute for Cancer Research<br/>Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,<br/>Brazil<br/>Tel: +55-11-2704922</p> |

Fax: +55-11-2707001  
Email: asimposon@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/getctm2.pl?tl=RC2&t=RC2-ET0188>)  
281100-013-g12&t3=2000-11-28&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 20  
High quality sequence stop: 489.

FEATURES  
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            /dev\_stage="Adult"  
            /note="Organ: lung\_tumor; Vector: puc18; Site\_1: SmaI;  
            Site\_2: SmaI; A mini-library was made by cloning products  
            derived from ORSTES PCR (U.S. Letters Patent application  
            No. 196,716 - Ludwig Institute for Cancer Research).

|                           |   |                    |           |             |  |  |  |
|---------------------------|---|--------------------|-----------|-------------|--|--|--|
|                           | tissue mRNA and cDNA amplification were performed under low stringency conditions." |                    |           |             |  |  |  |
| BASE COUNT                | 119 a   | 114 C              | 122 g     | 136 t       |  |  |  |
| ORIGIN                    |   |                    |           |             |  |  |  |
| Query Match               | 45..7%  | Score 228.8;       | DB 12;    | Length 491; |  |  |  |
| Best Local Similarity     | 99.1%;  | Pred. No. 1.1e-51; |           |             |  |  |  |
| Matches 230; Conservative | 0;  | Mismatches 2;      | Indels 0; | Gaps        |  |  |  |
| QY                        | 270 CAACCTGGCAGGACCGTGTGGGGCATCATCTACTTCACGCTACCTGCCCTACGCCTCCCT                    | 329                |           |             |  |  |  |
| Dd                        | 13 CAACCTGGCAGGACCGTGTGGGGCATCATCTACTTCACGCTACCTGCCCTACGCCT                         | 72                 |           |             |  |  |  |
| QY                        | 330 GTGTGTGGCAATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGTAGCCTGCTGTC                    | 389                |           |             |  |  |  |
| Dd                        | 73 GTGTGTGGCAATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGTAGCCTGCTGTC                     | 132                |           |             |  |  |  |
| QY                        | 390 TCCTGTGGCTTTTGSGTTTTGGCTGTGAQTATTGCCCTTTTAGGAGGACAGGSCATTGG                     | 449                |           |             |  |  |  |
| Dd                        | 133 TCCTGTGGCTTTTGSGTTTTGGCTGTGAQTATTGCCCTTTTAGGAGGACAGGSCATTGG                     | 192                |           |             |  |  |  |
| QY                        | 450 AGTCGAGTGGCACAACTGTTTGAGAGTCCTGCTGGAGCAATGGCTCCAAT                              | 501                |           |             |  |  |  |

|            |  |
|------------|--|
| RESULT     | 5  |
| BMI153383  |  |
| LOCUS      | BMI153383  |
| DEFINITION | TCPBPADJL1628 Pediatric pre-B cell acute lymphoblastic leukemia<br>Baylor HGSC project-TCBA Homo sapiens cDNA clone TCAP1162, mRNA sequence. |
| ACCESSION  | BMI153383  |

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VERSION      BM153383.1  GI:17178477
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,
JOURNAL      Pediatric Leukemia cDNA Sequencing Project (2001)
COMMENT      Unpublished (2001)
CONTACT: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@xccc.org
Seq primer: M13 primer.
FEATURES     Location/Qualifiers
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             /db_xref="taxon:9606"
             /clone="TCAP1162"
             /clone_lib="Pediatric pre-B cell acute lymphoblastic
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             /sex="male"
             /tissue_type="leukopheresis"
             /cell_type="pre-B cell"
             /dev_stage="pediatric 2 years"
             /lab_host="DH10B"
             note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
             First strand cDNA was primed with an anchored
             XhoI-oligo(dT) primer [5'GGAGACTCGCGCGCGAGGAG(T)VN
             3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand
             was primed with a BamHI-dC primer
             [5'AGAGCTCGGATCGCGCGCGCAATATATAT(C) 3'].
             Double-stranded cDNA was then digested with BamHI and XhoI
             and directionally cloned into the BamHI and SalI sites of
             lambda pSB vector. Library went through one round of
             normalization. Library was constructed by Wei Yu at RIKEN
             of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
             Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M,
             Schneider C, Hayashizaki Y, High efficiency selection of
             full-length cDNA by improved biotinylated cap trapper.,
             DNA Res 4: 1, 61-6, Feb 28, 1997)."
BASE COUNT   85 a 104 c 126 g 112 t
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Best Local Similarity 99.5%; Pred. No. 2.4e-45;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTGATCATCAGGGCATCGTGTATGAGAGGAGGAGCGGCTGAAGAGACCATCGGATC 60
DB 221 GTGATCATCAGGGCATCGTGTATGAGAGGAGGAGCGGCTGAAGAGACCATCGGATC 280
QY 61 ATGGGCGCTGGACACAGCATACTCTGTTTAGCTGGTTTACCTAGTACGCTATTCCTCTT 120
DB 281 ATGGGCGCTGGACACAGCATCTCTGTTTAGCTGGTTTACCTAGTACGCTATTCCTCTT 340
QY 121 CTTGTAGCGCTGGCGCTGCTAGTGGTTCATCTCTGTTAGTGAAGTGAAGACCTGCTGCCCTACAGT 180
DB 341 CTTGTAGCGCTGGCGCTGCTAGTGGTTCATCTCTGTTAGTGAAGTGAAGACCTGCTGCCCTACAGT 400
QY 181 GATCCACGCGGTGTTGTTCTTCCTG 207
DB 401 GATCCACGCGGTGTTGTTCTTCCTG 427
RESULT 6
BF928185/c
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Best Local Similarity 97.7%; Pred. No. 5.5e-43;
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QY 1 GTGATCATCAGGGCATCGTGTATGAGAGGAGGAGCGGCTGAAGAGACCATCGGATC 60
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QY 61 ATGGGCGCTGGACACAGCATCTCTGTTTAGCTGGTTTACCTAGTACGCTATTCCTCTT 120
DB 160 ATGGGCGCTGGACACAGCATCTCTGTTTAGCTGGTTTACCTAGTACGCTATTCCTCTT 101
QY 121 CTTGTAGCGCTGGCGCTGCTAGTGGTTCATCTCTGTTAGTGAAGTGAAGACCTGCTGCCCTACAGT 180
DB 100 CTTGTAGCGCTGCTAGTGGTTCATCTCTGTTAGTGAAGTGAAGACCTGCTGCCCTACAGT 42
QY 181 GATCCACGCGGTGTTGTTCTTCCTGCTCCGCTGTT 215
DB 41 GATCCACGCGGTGTTGTTCTTCCTGCTCCGCTGTT 7
RESULT 7
BF928185
LOCUS

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LOCUS U66691 2640 bp mRNA linear HTC 23-JUL-2001  
 DEFINITION Homo sapiens clone EST394388 mRNA sequence.  
 ACCESSION U66691  
 VERSION U66691.1 GI:1906576  
 KEYWORDS HTC.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 2640)  
 AUTHORS Allikmets, R., Gerrard, B., Hutchison, A. and Dean, M.  
 TITLE Characterization of the human ABC superfamily: isolation and  
 mapping of 21 new genes using the expressed sequence tags database  
 Hum. Mol. Genet. 5 (10), 1649-1655 (1996)  
 JOURNAL 97049974  
 MEDLINE  
 PUBMED 8894702  
 REFERENCE 2 (bases 1 to 2640)  
 AUTHORS Allikmets, R., Gerrard, B. and Dean, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer  
 Institute, NCI-FCRDC, Frederick, MD 21702, USA  
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 Db 41 TGNCTGTGAGAGCATCGACTATGAGAGAGGTGCGATCGAGAGACCTTGAAAAATC 100  
 QY 62 TGGCGCTGGACACAGACATCTGTGTTAGCTGGTTCATTAGTACCTCATCTCTCTTC 121  
 Db 101 AGGGTGTCTCCATCCAGCATGANTGTGTACCTGGTTCCTGGACANCTCTCCATCATGT 160  
 QY 122 TTGTGAGCGTGCCTGTAGTGTCTGATCTGCTGAAGTTAGTAACCTGCGCCCTACAGTG 181  
 Db 161 CGATGANCATCTTCTCTCCGCGATATTCATCATATGAGACATCCACATTCACAGC 220  
 QY 182 ATCCAGCGTGGTGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241  
 Db 221 ACCANTCATCT 280  
 QY 242 TCCTGATTACACATCTCTCTCAGAGCCAACTGCGAGCAGCAGCTGTGGGGCATCATCT 301  
 Db 281 TTCTGCTCAGACATCTCTCTCAGAGCCAACTGCGAGCAGCAGCTGTGGGGCATCATCT 340  
 QY 302 ACTTCAGCTGTACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
 Db 341 ATTTCACCTCTACCTCCACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400  
 QY 362 CACTCAAGATCTTCGCTAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421  
 Db 401 AGCTGNAGAGGCTGTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460  
 QY 422 TTGCGCTTTTGGAGGAGCGGATCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 481  
 Db 461 TGGTTCGCTTGAAGAGCAAGGCTGGGCTGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 520  
 QY 482 TGGAGGAGATGGCTTCA 499  
 Db 521 CGGAAGGGAGCAATTCA 538  
 RESULT 8  
 W29003/c

LOCUS W29003 850 bp mRNA linear EST 08-MAY-1996  
 DEFINITION 55g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA  
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 ACCESSION W29003  
 VERSION W29003.1 GI:1309023  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 850)  
 AUTHORS Macke, J., Smallwood, P. and Nathans, J.  
 TITLE Adult Human Retina cDNA  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Dr. Jeremy Nathans  
 Johns Hopkins School of Medicine  
 725 North Wolfe Street, Baltimore, MD 21205  
 Tel: 410 955 4678  
 Fax: 410 614 0827  
 Email: jeremy\_nathans@jhu.edu  
 Clones from this library are NOT available.  
 PCR Primers  
 FORWARD: CTTTGGAGCAAGTTACGCTGGTTAAGT  
 BACKWARD: GAGTGGCTATGATGATTTCTCCAGGGTAA  
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 sublibrary derived from a human retina cDNA library.  
 Inserts from retina cDNA library DNA were isolated,  
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 into lambda gt10. Individual plaques were arrayed and  
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 Db 578 TGAGAGGAGGTTGCGACTG-AGGAGACCTTGAATAATCAGGGTGCTCCAAATCCAGTGAN 520  
 QY 84 CTGGTTTACCTGGTTCATTAGTACCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 143  
 Db 519 TTGTTTACCTGGTTCCTGGACANCTTCTCCATCATGTGCGATGANCATCTTCTCTCTGCC 460  
 QY 144 GGTATCTCTGAAGTTAGGAAACCTGCTGCCATACAGTATCCAGCGTGGTGTGTTGCTT 203  
 Db 459 GATATTCATCATACATGAGNAGATCCNACATACACGACCCANTCATCTCTCTCTGTT 400  
 QY 204 CTGTCCGCTGTTTGT 263  
 Db 399 CTGTGTGGCTTTCTCCACTGCCACCATCATGCTGTGCTTCTGCTCAGCACCTTCTTCTC 340  
 QY 264 CAGAGCCACCTGGCAGCAGCTGTGGGCGATCATCTACTTACCTGCTACTGCTGCTGCTGCT 323  
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 QY 324 CGTCCCTGT 383  
 Db 279 CATCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 220



|    |  |      |   |      |
|----|--|------|---|------|
| Qy |  | 2    | TGATCATCAGGCATCTGTATGACAAGGACCGCTGAAGAGACCATCCGGATCA          | 61   |
|    |  |      |   |      |
| Dd |  | 1095 | TCATCTTGAGACCGTGGTCTATGAGAAGAGGC-CAGCTGAAGGAGACCATGAGGATCA    | 1037 |
|    |  |      |   |      |
| Qy |  | 62   | TGGSCCTGGACAACAGCATACTCTGTTTAGCTGGTTTCATTAGTAGCCCTCATTCCTCTTC | 121  |
|    |  |      |   |      |
| Dd |  | 1036 | TGGACTGAACAACAGGCATCCTGTGTGCAGCTGGTTTCATCAGCACGCCCTGGTYCCCTCC | 977  |
|    |  |      |   |      |
| Qy |  | 122  | TTGTGAGCGCTGGCCCTGCTAGTGGTTCATCTCTGAAGTT-----                 | 158  |
|    |  |      |   |      |
| Dd |  | 976  | TGATCAGCGCTGGACTGCTGGTGTCTGCTCAAGSTGAGAGGCTCTTTTCTCGGAGGT     | 917  |
|    |  |      |   |      |
| Qy |  | 159  | -----AGGA   | 162  |
|    |  |      |   |      |
| Dd |  | 916  | TC TT TGGAA CCGG GTCAGAACCGGGCTCCACCAGGCTCTCTGTCCTCAGAAAGG    | 857  |
|    |  |      |   |      |
| Qy |  | 163  | AACCTGCTGGCCCTACAGTGTATCCCAGCGTGGTGTGTTGTCTTCCTGCCGTTGTTGTGTG | 222  |
|    |  |      |   |      |
| Dd |  | 856  | AACCTGCTGCCCTACACGCAACCCAGGGGTGGTCTTCCTCTTCCTGGCCTCCTACGGTGTG | 797  |
|    |  |      |   |      |
| Qy |  | 223  | GTGACATCTCGAGTGCCTWCCCTGATTAGCACACTCTCTCCAGAGCCAACCTGGGACGA   | 282  |
|    |  |      |   |      |
| Dd |  | 796  | GTGACCATCATGCACTGCTTCTCTGCTCAGCAGCGCCCTCTCCCGGGCCACCTCTGGCGCG | 737  |
|    |  |      |   |      |
| Qy |  | 283  | GCCCTGTGGGGGCATCATCTTACTTCACGCTGTACOTGCCCTACGTCCTGTGTGTGGCANG | 342  |
|    |  |      |   |      |
| Dd |  | 736  | GCCCTGTGCGGGATCATCTACTTCACCCTCTACCTGGCCCTACGTGCTCTCGTGGCCTGG  | 677  |
|    |  |      |   |      |
| Qy |  | 343  | CAGGACTACGTGGGCTTCACACTCAAGATCTT                              | 374  |
|    |  |      |   |      |
| Dd |  | 676  | GAGGACTACATCGCTTCTCTCAGCCCAAAGTTGTT                           | 645  |
|    |  |      |   |      |

|            |   |              |               |                |                 |
|------------|---|--------------|---------------|----------------|-----------------|
| RESULT 11  | AZ721290  | 670 bp       | DNA           | linear         | GSS 24-JAN-2001 |
| LOCUS      | AZ721290  |              |               |                |                 |
| DEFINITION | RPCI-24-93E12.TV RPCI-24  | Mus musculus | genomic clone | RPCI-24-93E12, |                 |
|            | DNA sequence.   |              |               |                |                 |
| ACCESSION  | AZ721290  |              |               |                |                 |
| VERSION    | AZ721290  |              |               |                |                 |
| KEYWORDS   |   |              |               |                |                 |
| SOURCE     | AZ721290.1  | GI:12453834  |               |                |                 |
| ORGANISM   | GSS.  |              |               |                |                 |
|            | house mouse.  |              |               |                |                 |
|            | Mus musculus  |              |               |                |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;   |              |               |                |                 |
| AUTHORS    | Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  |              |               |                |                 |
|            | 1 (bases 1 to 670)  |              |               |                |                 |
|            | Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akınret, B., Levins, M.,  |              |               |                |                 |
|            | Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,   |              |               |                |                 |
|            | Russell, D., de Jong, P. and Fraser, C.M.   |              |               |                |                 |
| TITLE      | Mouse BAC End Sequences from Library RPCI-24  |              |               |                |                 |
| JOURNAL    | Unpublished (1999)  |              |               |                |                 |
| COMMENT    | Other_GSSs: RPCI-24-93E12.TJ  |              |               |                |                 |
|            | Contact: Shaying Zhao   |              |               |                |                 |
|            | Department of Eukaryotic Genomics   |              |               |                |                 |
|            | The Institute for Genomic Research  |              |               |                |                 |
|            | 9712 Medical Center Dr., Rockville, MD 20850, USA   |              |               |                |                 |
|            | Tel: 301 838 0200   |              |               |                |                 |
|            | Fax: 301 838 0208   |              |               |                |                 |
|            | Email: szhao@tigr.org   |              |               |                |                 |
|            | Clones are derived from the mouse BAC library RPCI-24. For BAC  |              |               |                |                 |
|            | library availability, please contact Pieter de Jong   |              |               |                |                 |
|            | (pdejong@mai.cho.org). Clones may be purchased from BACPAC  |              |               |                |                 |
|            | Resources ( <a href="http://www.choi.org/bacpac/orderingframe.htm">http://www.choi.org/bacpac/orderingframe.htm</a> ). BAC end          |              |               |                |                 |
|            | page: <a href="http://www.tigr.org/odb/bac_ends/mouse/bac_end_intro.html">http://www.tigr.org/odb/bac_ends/mouse/bac_end_intro.html</a> |              |               |                |                 |
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|            | Seq primer: T7  |              |               |                |                 |
|            | Class: BAC ends.  |              |               |                |                 |
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DNA."
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Qy 211 GTGTTTGTGTGGTGACAACTCTGCAGTGGCTTCTGATTAGCACACTCTTCTCCAGAGCC 270
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Qy 271 AACCTGGCAGCAG-CCTGTGGGGGCATCATCTACTTCA 307
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| ACCESSION  | BF928780  |        |      |        |                 |
| VERSION    | BF928780.1 GI:12336908  |        |      |        |                 |
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| SOURCE     | human.  |        |      |        |                 |
| ORGANISM   | Homo sapiens  |        |      |        |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.   |        |      |        |                 |
| AUTHORS    | 1 (bases 1 to 375)<br>Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., Geoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.J. |        |      |        |                 |
| TITLE      | Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  |        |      |        |                 |
| JOURNAL    | Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  |        |      |        |                 |
| MEDLINE    | 20202663  |        |      |        |                 |
| COMMENT    | Contact: Simpson A.J.G.   |        |      |        |                 |

Simpson,A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL56tJ=IL5-NT0228-061200-308-9056t3=2000-12-06&t4=1>)  
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FEATURES source

source

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Job time : 577.323 secs

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Best Local Similarity 51.6%; Pred. No. 1e-14;

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| RESULT 15  | AA772600  | LOCUS | AA772600 | 408 bp | mRNA | linear | EST 31-DEC-1998 |
| DEFINITION | ai30h01.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone 1358545 3', similar to SW:AB01_MOUSE P41233 ATP-BINDING CASSETTE TRANSPORTER 1 ; mRNA sequence. |       |          |        |      |        |                 |

TRANSFORMER 1.77 human sequence.

|           |              |
|-----------|--------------|
| ACCESSION | AA772600     |
| VERSION   | AA772600.1   |
| KEYWORDS  | GI:2824383   |
| SOURCE    | EST.         |
| ORGANISM  | human.       |
|           | Homo sapiens |

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Submitted (22/05/2004) by: Robert Strausberg, Ph.D.  
 Contact: Robert Strausberg, Ph.D.  
 Email: rsgabos-femail.nih.gov  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
 , Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio1.llnl.gov/brp/image/image.html](http://www-bio1.llnl.gov/brp/image/image.html)

possible reversed clone: similarity on wrong strand





GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 992.885 Seconds  
(without alignments)  
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Listing first 45 summaries

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| 6          | 501   | 100.0         | 10474  | 6     | AX060719 Sequence    |
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| 34         | 163.4 | 32.6          | 7323   | 9     | HSFA000148           |
| 35         | 155.4 | 31.0          | 7268   | 10    | MNAF000149           |
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ALIGNMENTS

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| RESULT 1   | AX092594  | AX092594    | 7860 bp | DNA | linear | PAT 21-MAR-2001 |
| LOCUS      | Sequence 6 from Patent WO0115676.   |             |         |     |        |                 |
| DEFINITION | Sequence 6 from Patent WO0115676.   |             |         |     |        |                 |
| ACCESSION  | AX092594  |             |         |     |        |                 |
| VERSION    | AX092594.1  | GI:13444651 |         |     |        |                 |
| KEYWORDS   | human.  |             |         |     |        |                 |
| SOURCE     | human.  |             |         |     |        |                 |
| ORGANISM   | Homo sapiens  |             |         |     |        |                 |
|            | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;                         |             |         |     |        |                 |
|            | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                      |             |         |     |        |                 |
| REFERENCE  | 1 (bases 1 to 7860)   |             |         |     |        |                 |
| AUTHORS    | Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.                    |             |         |     |        |                 |
| TITLE      | Compositions and methods for modulating hdl cholesterol and triglyceride levels |             |         |     |        |                 |

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0115676-A 6 08-MAR-2001;  
University of British Columbia (CA) ; Xenon Genetics Inc. (CA)  
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RESULT 2  
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DEFINITION Sequence 1 from Patent WO0132184.  
ACCESSION AX135712  
VERSION AX135712.1 GI:14271961  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 7862)  
AUTHORS Attie,A.D., Cook,M., Gray-Keller,M.P., Hayden,M.R., Pimstone,S. and Brooks-Wilson,A.  
TITLE Abcl modulation for the modulation of cholesterol transport  
JOURNAL Patent: WO 0132184-A 1 10-MAY-2001;  
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DB 4956 ATGGAATGTCAGTCTTCAATCATCCCTGATCTCACCAGGAGCAGCTCTCAGAG 5015  
QY 481 CTCTGATGACCATCATCAGTGG 501  
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DEFINITION Sequence 1 from Patent WO0078972.  
ACCESSION AX060713  
VERSION AX060713.1 GI:12406103  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 10442)  
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.  
TITLE Regulation with binding cassette transporter protein abcl  
JOURNAL Patent: WO 0078972-A 1 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
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source  
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RESULT 4
AX060892 10442 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0078971.
ACCESSION AX060892
VERSION AX060892.1 GI:12406270
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Law, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE Atp binding cassette transporter protein abc1 polypeptides
JOURNAL Patent: WO 0078971-A 1 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
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Best Local Similarity 100.0%; Pred. No. 9,8e-138;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 481 CTCTGATGACCAATCAGTGG 501
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Db 5230 CTCTGATGACCAATCAGTGG 5250

RESULT 5
AF285167 10442 bp mRNA linear PRI 09-AUG-2000
LOCUS
DEFINITION Homo sapiens ATP-binding cassette transporter 1 (ABCA1) mRNA,
complete cds.
ACCESSION AF285167
VERSION AF285167.1 GI:9755158
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Law, R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Porter, J.G., Sellhamer, J.J., Vaughan, A.M. and Oram, J.F.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
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BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others

Query Match 100.0%; Score 501; DB 9; Length 10442;  
Best Local Similarity 100.0%; Pred. No. 9.8e-138;  
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Db 5110 ATGTCATCAACAATGCCATTTCTCGGGCCAACTGCAAAAGGGAGAGAACCCCTAGCCATT 5169

QY 421 ATGGAATTACTGCTTCAATCATCCCTGAAATCTCACAAAGCAGCAGCTCTCAGAGGTGG 480  
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QY 481 CTCGTGATGACCAATCAGTGG 501  
Db 5230 CTCGTGATGACCAATCAGTGG 5250

RESULT 6  
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LOCUS  
DEFINITION Sequence 7 from Patent WO0078972.  
ACCESSION AX060719  
VERSION AX060719.1 GI:12406108  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 10474)  
AUTHORS Lawn, R.M., Wade, D. and Garvin, M.  
TITLE Regulation with binding cassette transporter protein abcl  
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
FEATURES  
Location/Qualifiers  
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BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others  
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Query Match 100.0%; Score 501; DB 6; Length 10474;  
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LOCUS  
DEFINITION Sequence 9 from Patent WO0078972.  
ACCESSION AX060721  
VERSION AX060721.1 GI:12406109  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10474)  
AUTHORS Lawn, R.M., Wade, D., and Garvin, M.  
TITLE Regulation with binding cassette transporter protein abcl  
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
FEATURES  
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AX060898 10474 bp DNA linear PAT 22-JAN-2001  
LOCUS Sequence 7 from Patent WO0078971.  
DEFINITION AX060898  
ACCESSION AX060898  
VERSION AX060898.1 GI:12406275  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10474)  
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.  
TITLE Atp binding cassette transporter protein abcl polypeptides  
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
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LOCUS Sequence 9 from Patent WO0078971.  
DEFINITION AX060900  
ACCESSION AX060900  
VERSION AX060900.1 GI:12406276  
KEYWORDS human.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10474)  
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.  
TITLE Atp binding cassette transporter protein abcl polypeptides  
JOURNAL Patent: WO 0078971-A 9 28-DEC-2000;  
CV THERAPEUTICS, INC. (US)  
FEATURES  
Location/Qualifiers  
source 1..10474  
BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others  
ORIGIN  
Query Match 100.0%; Score 501; DB 6; Length 10474;  
Best Local Similarity 100.0%; Pred. No. 9.8e-138;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 CTCTGATGACCAATCAGTGG 501
Db 5262 CTCTGATGACCAATCAGTGG 5282

RESULT 10
LOCUS AB055982
DEFINITION Homo sapiens mRNA for ABCA1, complete cds.
ACCESSION AB055982
VERSION AB055982.1 GI:15212106
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Tanaka,A.R., Abe-Dohmae,S., Arakawa,R., Sadanami,K., Kidera,A.,
Kioka,N., Amachi,T., Yokoyama,S. and Ueda,K.
A new topological model of functional human ABCA1-Signal peptide
cleavage and glycosylation of a large extracellular domain
Unpublished
2 (bases 1 to 6786)
Ueda,K., Kioka,N. and Tanaka,A.R.
Direct Submission
Submitted (20-FEB-2001) Kazumitsu Ueda, Kyoto University Graduate
School, Applied Life Sciences, Kitashirakawa, Kyoto Sakyo-ku, Kyoto
606-8502, Japan (E-mail:uedak@kais.kyoto-u.ac.jp,
Tel:81-75-753-6105, Fax:81-75-753-6104)
Location/Qualifiers
1. 6786
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DEFINITION Sequence 1 from Patent WO0170810.
ACCESSION AX253450
VERSION AX253450.1 GI:16073978
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SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6880)
Schmitz, G. and Bodzioch, M.
TITLE Atp binding cassette transporter 1 (abc1) gene polymorphisms and
uses thereof for the diagnosis and treatment of lipid,
cardiovascular or inflammatory disorders
JOURNAL Patent: WO 0170810-A 1 27-SEP-2001;
Bayer Aktiengesellschaft (DE)
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DEFINITION
ACCESSION AJ012376
VERSION AJ012376.1 GI:4128032
KEYWORDS ABC-1 gene; ATP-binding cassette transporter-1.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Langmann, T., Klucken, J., Reil, M., Liebisch, G., Luciani, M.F.,
Chimini, G., Kaminski, W. and Schmitz, G.
TITLE Molecular cloning of the human ATP-binding cassette transporter 1
(ABC1): evidence for sterol-dependent regulation in macrophages
JOURNAL Biochem. Biophys. Res. Commun. 257 (1), 29-33 (1999)
MEDLINE 99194549
PUBMED 10092505
REFERENCE
AUTHORS Langmann, T., Klucken, J., Reil, M., Liebisch, G., Luciani, M.F.,
Chimini, G., Kaminski, W. and Schmitz, G.
TITLE Molecular Cloning of the Human ATP-Binding Cassette Transporter 1
(ABC1): Evidence for Deterol-Dependent Regulation in Macrophages
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97, 7987-7992 (2000)
REFERENCE
AUTHORS Langmann, T.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1998) Langmann T., Institute for Clinical
Chemistry and Laboratory Medicine, University of Regensburg,
Franz-Josef-Strauss-Allee 11, 93053, GERMANY
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DEFINITION Sequence 3 from Patent WO0170810.  
ACCESSION AX253452  
VERSION AX253452.1 GI:16073979  
KEYWORDS

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 7260)  
AUTHORS Schmitz, G. and Bodisio, M.  
TITLE Atp binding cassette transporter 1 (abcl) gene polymorphisms and  
uses thereof for the diagnosis and treatment of lipid,  
cardiovascular or inflammatory disorders  
JOURNAL Patent: WO 0170810-A 3 27-SEP-2001;  
Bayer Aktiengesellschaft (DE)  
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ACCESSION AX059978  
VERSION AX059978.1 GI:12405636  
KEYWORDS  
SOURCE human.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 9495)  
AUTHORS Denefle, P., Rosier-Montus, M.F., Arnould-Requigne, I., Prades, C.,  
Naudin, L., Lemoine, C., Duverger, N., Assmann, G., Rust, S., Funke, H.



and Brewer,H.B.  
Nucleic and proteinic acids corresponding to human gene abcl  
Patent: WO 0078970-A 96 28-DEC-2000;  
Aventis Pharma S.A. (FR)  
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Best Local Similarity 99.6%; Pred. No. 8.7e-137;  
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REFERENCE 1 (bases 1 to 9497)  
AUTHORS Deneffe,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,  
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.  
and Brewer,H.B.  
TITLE Nucleic and proteinic acids corresponding to human gene abcl  
JOURNAL Patent: WO 0078970-A 91 28-DEC-2000;  
Aventis Pharma S.A. (FR)  
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DB 4400 CACAAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGGAGAAACATTTCCG 4459  
QY 61 ATTATCTGGTGAAGACGTATGTGCAGATCATGCCAAAAGCTTTAAAGAACAGATCTGGG 120  
DB 4460 ATTATCTGGTGAAGACGTATGTGCAGATCATGCCAAAAGCTTTAAAGAACAGATCTGGG 4519  
QY 121 TGAATGAGTTAGGTATGGCGCTTTTCCTGGGTGTCAGTAACTCAAGCACTTCCCTC 180  
DB 4520 TGAATGAGTTAGGTATGGCGCTTTTCCTGGGTGTCAGTAACTCAAGCACTTCCCTC 4579  
QY 181 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAACACCTAAAGCTGGCCAAAG 240  
DB 4580 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAACACCTAAAGCTGGCCAAAG 4639  
QY 241 ACAGTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
DB 4640 ACAGTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 4699  
QY 301 GAAATAATGTCAGAGTGTGGTTCAATAAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360  
DB 4700 GAAATAATGTCAGAGTGTGGTTCAATAAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 4759  
QY 361 ATGTATCAACAATGCCATTTCTCGGGCCAACTGCAAAAGGAGAGAACCCCTAGCCATT 420  
DB 4760 ATGTATCAACAATGCCATTTCTCGGGCCAACTGCAAAAGGAGAGAACCCCTAGCCATT 4819  
QY 421 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGAGCTCTCAGAGGTGG 480  
DB 4820 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGAGCTCTCAGAGGTGG 4879  
QY 481 CTCTGATGACCACATCAGTGG 501  
DB 4880 CTCCGATGACCACATCAGTGG 4900  
Search completed: April 3, 2003, 21:54:17  
Job time : 1040.89 secs



GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 84.2858 Seconds  
(without alignments)

13386.024 Million cell updates/sec

Title: US-09-595-526c-1\_COPY\_4750\_5250

Perfect score: 501

Sequence: 1 cacaagaagaaacaaacact.....tctgataccacatcagtg 501

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq.101002.\*

1: /SID52/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
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5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
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8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
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11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID          | Description        |
|------------|-------|-------------|--------|-------------|--------------------|
| 1          | 501   | 100.0       | 7857   | 21 AAC69388 | Human ABC1 cholest |
| 2          | 501   | 100.0       | 7860   | 22 AAF3826  | Human ABC1 nucleot |
| 3          | 501   | 100.0       | 7860   | 22 AAF2835  | Human ABC1 CDNA    |
| 4          | 501   | 100.0       | 7861   | 21 AAC69387 | Human ABC1 cholest |
| 5          | 501   | 100.0       | 7864   | 21 AAC69120 | Human ABC1 cholest |
| 6          | 501   | 100.0       | 7864   | 21 AAC69385 | Human ABC1 cholest |
| 7          | 501   | 100.0       | 7864   | 21 AAC69386 | Human ABC1 cholest |
| 8          | 501   | 100.0       | 7864   | 21 AAC69389 | Human ABC1 cholest |
| 9          | 501   | 100.0       | 10442  | 22 AAF24680 | Nucleotide sequenc |

|    |       |       |       |             |                    |
|----|-------|-------|-------|-------------|--------------------|
| 10 | 501   | 100.0 | 10442 | 22 AAF24702 | Nucleotide sequenc |
| 11 | 501   | 100.0 | 10474 | 22 AAF24685 | Nucleotide sequenc |
| 12 | 501   | 100.0 | 10474 | 22 AAF24686 | Nucleotide sequenc |
| 13 | 501   | 100.0 | 10474 | 22 AAF24707 | Nucleotide sequenc |
| 14 | 501   | 100.0 | 10474 | 22 AAF24708 | Nucleotide sequenc |
| 15 | 497.8 | 99.4  | 6880  | 21 AAZ94734 | Human ATP binding  |
| 16 | 497.8 | 99.4  | 6880  | 22 AAD21325 | Human ATP binding  |
| 17 | 497.8 | 99.4  | 6880  | 22 AAI70314 | Human ATP binding  |
| 18 | 497.8 | 99.4  | 7086  | 22 ABA09200 | Human ABCA1 homolo |
| 19 | 497.8 | 99.4  | 7086  | 22 AAK52667 | Human polynucleoti |
| 20 | 497.8 | 99.4  | 7260  | 22 AAD21326 | Human ATP binding  |
| 21 | 497.8 | 99.4  | 7260  | 22 AAI70315 | Human ATP binding  |
| 22 | 497.8 | 99.4  | 7281  | 22 AAK51683 | Human polynucleoti |
| 23 | 497.8 | 99.4  | 9741  | 22 AAS06120 | Human ABC1 DNA seq |
| 24 | 497.8 | 99.4  | 9741  | 24 AAD37273 | Human ABC1 full-le |
| 25 | 497.8 | 99.4  | 9854  | 22 AAS06121 | Human ABC1 DNA seq |
| 26 | 173   | 34.5  | 6289  | 21 AAC69144 | Human ABC1 gene ex |
| 27 | 173   | 34.5  | 18399 | 22 AAF92831 | Human ABC1 genomic |
| 28 | 163.4 | 32.6  | 7323  | 21 AAZ94746 | Human ATP binding  |
| 29 | 163.4 | 32.6  | 7784  | 19 AAV33392 | ATP binding casses |
| 30 | 142   | 28.3  | 399   | 22 AAI81212 | Human polynucleoti |
| 31 | 139.4 | 27.8  | 5669  | 22 AAS08707 | Human PD-ATP-bindi |
| 32 | 139.4 | 27.8  | 6522  | 22 AAS08706 | Human PD-ATP-bindi |
| 33 | 137.8 | 27.5  | 2911  | 21 AAZ94751 | Human ATP binding  |
| 34 | 137.8 | 27.5  | 3437  | 23 AAF73965 | DNA encoding novel |
| 35 | 137.8 | 27.5  | 3635  | 22 AAF56389 | ABC transport rela |
| 36 | 137.8 | 27.5  | 4413  | 23 AAS37115 | DNA encoding novel |
| 37 | 137.8 | 27.5  | 5811  | 22 AAD05626 | Human secreted pro |
| 38 | 137.8 | 27.5  | 6768  | 24 AAS19207 | DNA encoding human |
| 39 | 137.8 | 27.5  | 7795  | 24 ABL57810 | Human ABCA7 coding |
| 40 | 136.2 | 27.2  | 6791  | 24 AAL44693 | Human transporter  |
| 41 | 132.4 | 26.4  | 5762  | 22 AAF4792  | Nucleotide sequenc |
| 42 | 132.4 | 26.4  | 5607  | 22 AAF4812  | Nucleotide sequenc |
| 43 | 98.2  | 19.6  | 2841  | 21 AAC69142 | Human ABC1 gene ex |
| 44 | 82    | 16.4  | 669   | 22 AAO08356 | Human cDNA clone ( |
| 45 | 82    | 16.4  | 5097  | 22 AAI93913 | Human stomach canc |

#### ALIGNMENTS

#### RESULT 1

AAC69388

ID AAC69388 standard; cDNA; 7857 BP.

AC AAC69388;

DT 29-JAN-2001 (first entry)

XX Human ABC1 cholesterol transporter FHA-3 mutant cDNA (delta 5752-5757).

XX Human ABC1 cholesterol transporter; chromosome 9q31;

XX ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;

XX Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;

XX cardiovascular disease; coronary artery disease; coronary restenosis;

XX cerebrovascular disease; peripheral vascular disease;

XX Alzheimer's disease; Niemann-Pick disease; Huntington's disease;

XX X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;

XX prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.

OS Homo sapiens.

XX WO200005318-A2.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-IB00532.

XX 15-MAR-1999; 99US-0124702.

XX 08-JUN-1999; 99US-0138048.

XX 17-JUN-1999; 99US-0139600.

XX 01-SEP-1999; 99US-0151977.

PA (UYBR-) UNIV BRITISH COLUMBIA.  
PI (XENO-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Pimstone SN;  
PI

XX WPI; 2000-587528/55.  
DR P-PSDB; AAB38107.

XX New ABC1 polypeptide is useful for treating diseases associated with  
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
PT disease and cancer  
XX

XX Examples; Page -: 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein  
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
CC proteins, and plays a crucial role in cholesterol transport, particularly  
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
CC located on chromosome 9q31, and mutations in this gene are associated  
CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
CC are distinguishable in that TD is an autosomal recessive disorder, while  
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
CC cholesterol") in the blood correlate with a high risk of cardiovascular  
CC disease, particularly coronary artery disease, but also cerebrovascular  
CC disease, coronary stenosis, and peripheral vascular disease.  
CC Conversely, a high level of HDL has protective effects against  
CC cardiovascular disease. The invention provides genetic constructs and  
CC transgenic cells and non-human animals comprising human ABC1 nucleic  
CC acids, and methods of gene therapy for the treatment or prevention of  
CC cardiovascular disease comprising the administration of an expression  
CC vector encoding ABC1 or an active fragment thereof. The invention also  
CC encompasses compounds which mimic ABC1 activity, compounds which  
CC stimulate ABC1 expression and methods of screening for such compounds.  
CC It further relates to methods for determining whether a patient has an  
CC increased risk for cardiovascular disease due to polymorphisms in the  
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
CC or prevent cardiovascular disease, especially coronary artery disease,  
CC cerebrovascular disease, coronary stenosis or peripheral vascular  
CC disease. They may also be used in the treatment of diseases associated  
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
CC The invention specifically excludes proteins with the exact amino acid  
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
CC acid with the exact sequence as GenBank Accession No: A012376.1. The  
CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
CC transporter associated with an altered cholesterol level and therefore an  
CC altered risk of cardiovascular disease.  
CC Note: The present sequence is not shown in the specification, but is  
CC derived from the native human ABC1 cDNA shown on pages 157-160.

XX Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;

Query Match 100.0%; Score 501; DB 21; Length 7857;  
Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAAGAAACAAACACTGCAGATATCTTCAGGACCTCACAGGAAGAACATTTGGG 60

DB 4537 CACAAGAAACAAACACTGCAGATATCTTCAGGACCTCACAGGAAGAACATTTGGG 4596

QY 61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 120

DB 4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 4656

QY 121 TGAATGAGTTTGGTATGGCGCTTTCCCTGGGTGTCAGTAATACATCAACACTTCTC 180

DB 4657 TGAATGAGTTTGGTATGGCGCTTTCCCTGGGTGTCAGTAATACATCAACACTTCTC 4716

QY 181 CGAGTCAAGAACTTAATGATGCATCAACAAATGAACAAACACTTAAGCTGGCCAAAG 240

DB 4717 CGAGTCAAGAACTTAATGATGCATCAACAAATGAACAAACACTTAAGCTGGCCAAAG 4776  
QY 241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGCAAGATTTATGACAGGACTGACACCA 300  
DB 4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGCAAGATTTATGACAGGACTGACACCA 4836  
QY 301 GAAATAATGTCAAGGTGTGGTTCAATAACAGGGCTGGCATGCAATCAGCTCTTCTCTGA 360  
DB 4837 GAAATAATGTCAAGGTGTGGTTCAATAACAGGGCTGGCATGCAATCAGCTCTTCTCTGA 4896  
QY 361 ATGTCATCAACAATGCCATTCTCGGGCCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 420  
DB 4897 ATGTCATCAACAATGCCATTCTCGGGCCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 4956  
QY 421 ATGGAATTACTGCTTTCAATCATCCCTGTAATCTCACCAGCAGCAGCTCTCAGAGGTGG 480  
DB 4957 ATGGAATTACTGCTTTCAATCATCCCTGTAATCTCACCAGCAGCAGCTCTCAGAGGTGG 5016  
QY 481 CTCGTGATGACCATCATCAGTGG 501  
DB 5017 CTCGTGATGACCATCATCAGTGG 5037

# RESULT 2

AAF83826 standard; DNA; 7860 BP.

AAF83826;

06-AUG-2001 (first entry)

Human ABC1 nucleotide sequence.

ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;  
LDL; ds.

Homo sapiens.

Key Location/Qualifiers  
CDS 75..3341

/product= "partial ABC1 protein"

/note= "the coding sequence continues beyond nucleotide  
3341, possibly till position 6860 as identified  
by translating the present sequence; part of the  
corresponding protein is missing and nucleotide  
3341 corresponds to the last amino acid residue  
(position 1089) as indicated in the  
specification"

W0200132184-A2.

10-MAY-2001.

01-NOV-2000; 2000WO-US030109.

01-NOV-1999; 99US-0162803.

30-JUN-2000; 2000US-0215564.

(WISC ) WISCONSIN ALUMNI RES FOUND.

Attie AD, Cook M, Gray-Keller MP, Hayden MR, Pimstone S;  
Brooks-Wilson A;

WPI; 2001-335779/35.

P-PSDB; AAB62691.

New method for inhibiting cholesterol uptake in the gut comprises  
administration of an inhibitor of an ABC1 protein

Disclosure; Page 34-36; 41pp; English.

The invention relates to a new method for inhibiting cholesterol uptake

CC in the gut that comprises administration of an inhibitor of an ABCI  
 CC protein. The method is useful for: lowering levels of LDL (low density  
 CC lipoprotein) cholesterol by reducing the activity of ABCI protein in the  
 CC intestinal cells and the abundance of the ABCI protein in the individual  
 CC by inhibiting the activity of the protein; identifying drugs that can  
 CC lower serum cholesterol and LDL levels comprising assaying the drug to  
 CC test if it can bind to an ABCI protein; testing LDL cholesterol lowering  
 CC agents; and for modulation of ABCI biological activity. The present  
 CC sequence represents a human ABCI nucleotide sequence.

XX SQ Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;

Query Match 100.0%; Score 501; DB 22; Length 7860;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGAGAGAAACATTTGGG 60  
 DB 4534 CACAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGAGAGAAACATTTGGG 4593  
 QY 61 ATTATCTGCTGAAGAGTATGTCAGATCATAGCCAAAGCTTAAAGACAAAGATCTGGG 120  
 DB 4594 ATTATCTGCTGAAGAGTATGTCAGATCATAGCCAAAGCTTAAAGACAAAGATCTGGG 4653  
 QY 121 TGAATCAGTTTATGATGCGGCTTTTCCTGGGTCTCAGTAACTCAAGCACTTCCTC 180  
 DB 4654 TGAATCAGTTTATGATGCGGCTTTTCCTGGGTCTCAGTAACTCAAGCACTTCCTC 4713  
 QY 181 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGCTGGCCNAGG 240  
 DB 4714 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGCTGGCCNAGG 4773  
 QY 241 ACAGTTCTCAGATCATGATTTCAACAGCTTGGGAGATTTATGACAGGACTGGACACCA 300  
 DB 4774 ACAGTTCTCAGATCATGATTTCAACAGCTTGGGAGATTTATGACAGGACTGGACACCA 4833  
 QY 301 GAAATTAATGTCAGGTTGGTTCAATAACAAGGCTGGCATGCAATCAGCTCTTTCCTGA 360  
 DB 4834 GAAATTAATGTCAGGTTGGTTCAATAACAAGGCTGGCATGCAATCAGCTCTTTCCTGA 4893  
 QY 361 ATGTCATCAACAAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 420  
 DB 4894 ATGTCATCAACAAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 4953  
 QY 421 CTCTGATGACCATCAGTGG 501  
 DB 5014 CTCTGATGACCATCAGTGG 5034

RESULT 3  
 AAF92835  
 ID AAF92835 standard; DNA; 7860 BP.  
 XX AC AAF92835;

XX DT 17-MAY-2001 (first entry)

XX DE Human ABCI cDNA.

XX KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABCI; ss.

XX OS Homo sapiens.

XX PN WO200115676-A2.

XX PD 08-MAR-2001.

XX PF 01-SEP-2000; 2000WO-1B01492.

XX

PR 01-SEP-1999; 99US-0151977.  
 PR 15-MAR-2000; 2000US-0526193.  
 PR 23-JUN-2000; 2000US-0213958.  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 PA (XENO-) XENON GENETICS INC.  
 XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;  
 DR WPI; 2001-244356/25.

PT Treating a lower than normal high density lipoprotein-cholesterol  
 PT (HDL-C) level, a higher than normal triglyceride level, or a  
 PT cardiovascular disease, by administering a compound that modulates LXR-  
 PT or RXR-mediated transcriptional activity -

XX Disclosure; Fig 2; 317pp; English.

PS The present invention relates to a method for treating a patient  
 CC diagnosed as having a lower than normal high density  
 CC lipoprotein-cholesterol (HDL-C) level, a higher than normal  
 CC triglyceride level, or a cardiovascular disease, involving  
 CC administering a compound that modulates LXR- or RXR-mediated  
 CC transcriptional activity or ABCI expression or activity.  
 CC The LXR gene product may be used in an assay to identify  
 CC compounds useful for the treatment of a disease or condition selected a  
 CC lower than normal HDL cholesterol level, a higher than normal  
 CC triglyceride level, and a cardiovascular disease.

XX SQ Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;

Query Match 100.0%; Score 501; DB 22; Length 7860;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGAGAGAAACATTTGGG 60  
 DB 4534 CACAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGAGAGAAACATTTGGG 4593  
 QY 61 ATTATCTGCTGAAGAGTATGTCAGATCATAGCCAAAGCTTAAAGACAAAGATCTGGG 120  
 DB 4594 ATTATCTGCTGAAGAGTATGTCAGATCATAGCCAAAGCTTAAAGACAAAGATCTGGG 4653  
 QY 121 TGAATCAGTTTATGATGCGGCTTTTCCTGGGTCTCAGTAACTCAAGCACTTCCTC 180  
 DB 4654 TGAATCAGTTTATGATGCGGCTTTTCCTGGGTCTCAGTAACTCAAGCACTTCCTC 4713  
 QY 181 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGCTGGCCNAGG 240  
 DB 4714 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGCTGGCCNAGG 4773  
 QY 241 ACAGTTCTCAGATCATGATTTCAACAGCTTGGGAGATTTATGACAGGACTGGACACCA 300  
 DB 4774 ACAGTTCTCAGATCATGATTTCAACAGCTTGGGAGATTTATGACAGGACTGGACACCA 4833  
 QY 301 GAAATTAATGTCAGGTTGGTTCAATAACAAGGCTGGCATGCAATCAGCTCTTTCCTGA 360  
 DB 4834 GAAATTAATGTCAGGTTGGTTCAATAACAAGGCTGGCATGCAATCAGCTCTTTCCTGA 4893  
 QY 361 ATGTCATCAACAAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 420  
 DB 4894 ATGTCATCAACAAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 4953  
 QY 421 ATGGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 480  
 DB 4954 ATGGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 5013  
 QY 481 CTCTGATGACCATCAGTGG 501  
 DB 5014 CTCTGATGACCATCAGTGG 5034

RESULT 4

AAC69387  
ID AAC69387 standard; cDNA; 7861 BP.  
XX AC AAC69387;  
XX AC AAC69387;  
XX DT 29-JAN-2001 (first entry)  
XX DE Human ABC1 cholesterol transporter FHA-1 mutant cDNA (delta 2151-2153).  
XX DE Human ABC1 cholesterol transporter; chromosome 9q31;  
XX KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
XX KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
XX KW cardiovascular disease; coronary artery disease; coronary stenosis;  
XX KW cerebrovascular disease; peripheral vascular disease;  
XX KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
XX KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
XX KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.  
XX OS Homo sapiens.  
XX PN WO20005318-A2.  
XX PD 21-SEP-2000.  
XX PF 15-MAR-2000; 2000WO-IB00532.  
XX PR 15-MAR-1999; 99US-0124702.  
XX PR 08-JUN-1999; 99US-0138048.  
XX PR 17-JUN-1999; 99US-0139600.  
XX PR 01-SEP-1999; 99US-0151977.  
XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX PA (XENO-) XENON BIORESEARCH INC.  
XX PI Hayden MR, Wilson AR, Pimstone SN;  
XX WPI: 2000-587528/55.  
XX P-PSDB; AAB38106.  
XX PT New ABC1 polypeptide is useful for treating diseases associated with  
XX PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
XX PT disease and cancer -  
XX PS Examples; Page -: 229pp; English.  
XX CC The invention relates to the human ABC1 cholesterol transporter protein  
XX CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
XX CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
XX CC proteins, and plays a crucial role in cholesterol transport, particularly  
XX CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
XX CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
XX CC located on chromosome 9q31, and mutations in this gene are associated  
XX CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
XX CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
XX CC are distinguishable in that TD is an autosomal recessive disorder, while  
XX CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
XX CC cholesterol") in the blood correlate with a high risk of cardiovascular  
XX CC disease, particularly coronary artery disease, but also cerebrovascular  
XX CC disease, coronary stenosis, and peripheral vascular disease.  
XX CC Conversely, a high level of HDL has protective effects against  
XX CC cardiovascular disease. The invention provides genetic constructs and  
XX CC transgenic cells and non-human animals comprising human ABC1 nucleic  
XX CC acids, and methods of gene therapy for the treatment or prevention of  
XX CC cardiovascular disease comprising the administration of an expression  
XX CC vector encoding ABC1 or an active fragment thereof. The invention also  
XX CC encompasses compounds which mimic ABC1 activity, compounds which  
XX CC stimulate ABC1 expression and methods of screening for such compounds.  
XX CC It further relates to methods for determining whether a patient has an  
XX CC increased risk for cardiovascular disease due to polymorphisms in the  
XX CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
XX CC or prevent cardiovascular disease, especially coronary artery disease,  
XX CC cerebrovascular disease, coronary stenosis or peripheral vascular  
XX CC disease. They may also be used in the treatment of diseases associated

with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
The invention specifically excludes proteins with the exact amino acid  
sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
transporter associated with an altered cholesterol level and therefore an  
altered risk of cardiovascular disease.  
Note: The present sequence is not shown in the specification, but is  
derived from the native human ABC1 cDNA shown on pages 157-160.  
SQ Sequence 7861 BP; 2014 A; 1859 C; 2011 G; 1976 T; 1 other;  
Query Match 100.0%; Score 501; DB 21; Length 7861;  
Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CACAAAGAAAACACACTGCAGATATCTTCAGGACCTGACAGGAGAAACATTCGG 60  
DB 4534 CACAAAGAAAACACACTGCAGATATCTTCAGGACCTGACAGGAGAAACATTCGG 4593  
OY 61 ATTATCTGGTGAAGACGCTATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGG 120  
DB 4594 ATTATCTGGTGAAGACGCTATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGG 4653  
OY 121 TGAATGAGTTTAGTATGGCGCTTTTCCCTGGGTGTCAGTACTCAAGCACTTCCTC 180  
DB 4654 TGAATGAGTTTAGTATGGCGCTTTTCCCTGGGTGTCAGTACTCAAGCACTTCCTC 4713  
OY 181 CGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAAACACCTTAAAGCTGCCAAG 240  
DB 4714 CGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAAACACCTTAAAGCTGCCAAG 4773  
OY 241 ACAGTCTGCAGATCGATTTCTCAACAGCTTGGAGAGATTATGACAGGACTGGACCA 300  
DB 4774 ACAGTCTGCAGATCGATTTCTCAACAGCTTGGAGAGATTATGACAGGACTGGACCA 4833  
OY 301 GAAATAATGCAAGGTGTGGTTCAATAACAGGCTGGCATGCAATCAGCTCTTCTCTGA 360  
DB 4834 GAAATAATGCAAGGTGTGGTTCAATAACAGGCTGGCATGCAATCAGCTCTTCTCTGA 4893  
OY 361 ATGTCATCAACATGCCATTCCTCGGCGCAACCTGCAAGAGGAGAGACCCCTAGCAAT 420  
DB 4894 ATGTCATCAACATGCCATTCCTCGGCGCAACCTGCAAGAGGAGAGACCCCTAGCAAT 4953  
OY 421 ATGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGCAGCTCTCAGAGGTGG 480  
DB 4954 ATGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGCAGCTCTCAGAGGTGG 5013  
OY 481 CTCTGATGACCATCATCAGTGG 501  
DB 5014 CTCTGATGACCATCATCAGTGG 5034  
RESULT 5  
AAC69120  
ID AAC69120 standard; cDNA; 7864 BP.  
XX AC AAC69120;  
XX DT 29-JAN-2001 (first entry)  
XX DE Human ABC1 cholesterol transporter cDNA.  
XX KW Human ABC1 cholesterol transporter; chromosome 9q31;  
XX KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
XX KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
XX KW cardiovascular disease; coronary artery disease; coronary stenosis;  
XX KW cerebrovascular disease; peripheral vascular disease;  
XX KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
XX KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
XX KW prognosis; prophylaxis; drug screening; transgenic animal; ss.

OS Homo sapiens.  
 XX WO200055318-A2.  
 XX  
 XX 21-SEP-2000.  
 XX  
 XX 15-MAR-2000; 2000WO-IB00532.  
 XX  
 XX 15-MAR-1999; 99US-0124702.  
 XX 08-JUN-1999; 99US-0138048.  
 XX 17-JUN-1999; 99US-0139600.  
 XX 01-SEP-1999; 99US-0151977.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 XX WPI; 2000-587528/55.  
 XX P-PSDB; AAB38082.  
 XX  
 XX New ABC1 polypeptide is useful for treating diseases associated with  
 XX ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
 XX disease and cancer -  
 XX  
 XX Claim 13; Page 157-160; 229pp; English.  
 XX  
 XX The invention relates to the human ABC1 cholesterol transporter protein  
 XX (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
 XX a member of the ATP-binding cassette (ABC transporter) superfamily of  
 XX proteins, and plays a crucial role in cholesterol transport, particularly  
 XX intracellular cholesterol trafficking in monocytes and fibroblasts, being  
 XX involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
 XX located on chromosome 9q31, and mutations in this gene are associated  
 XX with two genetic HDL (high density lipoprotein) deficiency disorders,  
 XX Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
 XX are distinguishable in that TD is an autosomal recessive disorder, while  
 XX FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
 XX cholesterol") in the blood correlate with a high risk of cardiovascular  
 XX disease, particularly coronary artery disease, but also cerebrovascular  
 XX disease, coronary restenosis, and peripheral vascular disease.  
 XX Conversely, a high level of HDL has protective effects against  
 XX cardiovascular disease. The invention provides genetic constructs and  
 XX transgenic cells and non-human animals comprising human ABC1 nucleic  
 XX acids, and methods of gene therapy for the treatment or prevention of  
 XX cardiovascular disease comprising the administration of an expression  
 XX vector encoding ABC1 or an active fragment thereof. The invention also  
 XX encompasses compounds which mimic ABC1 activity, compounds which  
 XX stimulate ABC1 expression and methods of screening for such compounds.  
 XX It further relates to methods for determining whether a patient has an  
 XX increased risk for cardiovascular disease due to polymorphisms in the  
 XX ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
 XX or prevent cardiovascular disease, especially coronary artery disease,  
 XX cerebrovascular disease, coronary restenosis or peripheral vascular  
 XX disease. They may also be used in the treatment of diseases associated  
 XX with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
 XX disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
 XX The invention specifically excludes proteins with the exact amino acid  
 XX sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 XX acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 XX present sequence represents cDNA encoding the human ABC1 cholesterol  
 XX transporter.

Query Match 100.0%; Score 501; DB 21; Length 7864;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CACAAAGAAACAAACACTGCAGATATCTTCAGGACCTGCAGAGGAAACATTCGG 60  
 4537 CACAAAGAAACAAACACTGCAGATATCTTCAGGACCTGCAGAGGAAACATTCGG 4596

QY 61 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAGAAACAAGATCTGGG 120  
 Db 4597 ATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAGAAACAAGATCTGGG 4656  
 QY 121 TGAATGAGTTAGCTATGGCGGCTTTCCCTGGGTGTCAGTAAATACCTCAAGCACTTCCTC 180  
 Db 4657 TGAATGAGTTAGCTATGGCGGCTTTCCCTGGGTGTCAGTAAATACCTCAAGCACTTCCTC 4716  
 QY 181 CGAGTCAAGAAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGTGCCCAAGG 240  
 Db 4717 CGAGTCAAGAAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGTGCCCAAGG 4776  
 QY 241 ACAGTTCTGAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGCACACCA 300  
 Db 4777 ACAGTTCTGAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGCACACCA 4836  
 QY 301 GAAATATGTCAAGGTGTGGTTCAATCAACAAGGGCTGCATGCAATCAGCTCTTCCTGA 360  
 Db 4837 GAAATATGTCAAGGTGTGGTTCAATCAACAAGGGCTGCATGCAATCAGCTCTTCCTGA 4896  
 QY 361 ATGTCATCAACAATGCCATTCTCGGGCCAACTGCAAAAGGGAGAGAACCTTAGCCATT 420  
 Db 4897 ATGTCATCAACAATGCCATTCTCGGGCCAACTGCAAAAGGGAGAGAACCTTAGCCATT 4956  
 QY 421 ATGGAATTACTGCTTTCATCATCCCTGGAATCTCACCACGACGCTCTCAGAGGTGG 480  
 Db 4957 ATGGAATTACTGCTTTCATCATCCCTGGAATCTCACCACGACGCTCTCAGAGGTGG 5016  
 QY 481 CTCTGATGACCAATCAATCAATGTTG 501  
 Db 5017 CTCTGATGACCAATCAATCAATGTTG 5037  
 RESULT 6  
 AAC69385  
 ID AAC69385 standard; cDNA; 7864 BP.  
 AC AAC69385;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human ABC1 cholesterol transporter TD-1 mutant cDNA (T4503C).  
 KW Human ABC1 cholesterol transporter; chromosome 9q31;  
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
 KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
 KW cardiovascular disease; coronary artery disease; coronary restenosis;  
 KW cerebrovascular disease; peripheral vascular disease;  
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
 KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.  
 OS Homo sapiens.  
 XX WO200055318-A2.  
 XX 21-SEP-2000.  
 XX 15-MAR-2000; 2000WO-IB00532.  
 XX 15-MAR-1999; 99US-0124702.  
 XX 08-JUN-1999; 99US-0138048.  
 XX 17-JUN-1999; 99US-0139600.  
 XX 01-SEP-1999; 99US-0151977.  
 XX  
 XX (UYBR-) UNIV BRITISH COLUMBIA.  
 XX (XENO-) XENON BIORESEARCH INC.  
 XX  
 XX Hayden MR, Wilson AR, Pimstone SN;  
 XX  
 XX WPI; 2000-587528/55.  
 XX P-PSDB; AAB38104.

New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's disease and cancer -

Examples; Page -: 229pp; English.

The invention relates to the human ABC1 cholesterol transporter protein (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-binding cassette (ABC transporter) superfamily of proteins, and plays a crucial role in cholesterol transport, particularly intracellular cholesterol trafficking in monocytes and fibroblasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders, Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive disorder, while FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good cholesterol") in the blood correlate with a high risk of cardiovascular disease, particularly coronary artery disease, but also cerebrovascular disease, coronary restenosis, and peripheral vascular disease. Conversely, a high level of HDL has protective effects against cardiovascular disease. The invention provides genetic constructs and transgenic cells and non-human animals comprising human ABC1 nucleic acids, and methods of gene therapy for the treatment or prevention of cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also encompasses compounds which mimic ABC1 activity, compounds which stimulate ABC1 expression and methods of screening for such compounds. It further relates to methods for determining whether a patient has an increased risk for cardiovascular disease due to polymorphisms in the ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or prevent cardiovascular disease, especially coronary artery disease, cerebrovascular disease, coronary restenosis or peripheral vascular disease. They may also be used in the treatment of diseases associated with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer. The invention specifically excludes proteins with the exact amino acid sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic acid with the exact sequence as GenBank Accession No: A012376.1. The present sequence represents cDNA encoding a mutant human ABC1 cholesterol transporter associated with an altered cholesterol level and therefore an altered risk of cardiovascular disease.

Note: The present sequence is not shown in the specification, but is derived from the native human ABC1 cDNA shown on pages 157-160.

Sequence 7864 BP; 2014 A; 1861 C; 2011 G; 1977 T; 1 other;

Query Match 100.0%; Score 501; DB 21; Length 7864;  
Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CACAAGAAACAACTGCAGATATCCCTTCAGGACCTGACAGGAGAAACATTTCCG 60  
|||||  
4537 CACAAGAAACAACTGCAGATATCCCTTCAGGACCTGACAGGAGAAACATTTCCG 4596  
|||||

61 ATTATCTGGTGAAGACGATGTGAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 120  
|||||

4597 ATTATCTGGTGAAGACGATGTGAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 4656  
|||||

121 TGAATGAGTTAGGTGATGGGGCTTTCCCTGGGTGTCAGTAATCAAGCACTTCCTC 180  
|||||

4657 TGAATGAGTTAGGTGATGGGGCTTTCCCTGGGTGTCAGTAATCAAGCACTTCCTC 4716  
|||||

181 CGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAACACCTAAAGCTGGCCCAAGG 240  
|||||

4717 CGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAACACCTAAAGCTGGCCCAAGG 4776  
|||||

241 ACAGTCTGCAGTCGATTTCTACAGCTTGGGAAGATTATACAGGACTGGACACCA 300  
|||||

4777 ACAGTCTGCAGTCGATTTCTACAGCTTGGGAAGATTATACAGGACTGGACACCA 4836  
|||||

301 GAAATAATGTCAAGGTGGTTTCAATACAAAGGGCTGCATGCAATCAGCTCTTTCTCTGA 360  
|||||

Db 4837 GAAATAATGTCAAGGTGGTTTCAATACAAAGGGCTGCATGCAATCAGCTCTTTCTCTGA 4896  
QY 361 ATGTCATCAACAATGCCAATCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 420  
|||||  
Db 4897 ATGTCATCAACAATGCCAATCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 4956  
QY 421 ATGGAATTAATGCTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 480  
|||||  
Db 4957 ATGGAATTAATGCTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 5016  
QY 481 CTCGTGATGACCACATCATGCTGG 501  
|||||  
Db 5017 CTCGTGATGACCACATCATGCTGG 5037  
|||||

#### RESULT 7

AAC69386  
ID AAC69386 standard; cDNA; 7864 BP.

XX AAC69386;

XX 29-JAN-2001 (first entry)

XX Human ABC1 cholesterol transporter TD-2 mutant cDNA (A1864G).

XX Human ABC1 cholesterol transporter; chromosome 9q31;  
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
KW Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
KW cerebrovascular disease; coronary artery disease; coronary restenosis;  
KW cerebrovascular disease; peripheral vascular disease;  
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.

OS Homo sapiens.

XX WO200055318-A2.

XX 21-SEP-2000.

XX 15-MAR-2000; 2000WO-IB00532.

XX 15-MAR-1999; 99US-0124702.

XX 08-JUN-1999; 99US-0138048.

XX 17-JUN-1999; 99US-0139600.

XX 01-SEP-1999; 99US-0151977.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX (XENO-) XENON BIORESEARCH INC.

XX Hayden MR, Wilson AR, Pimstone SN;

XX WPI; 2000-587528/55.

XX P-PSDB; AAB38105.

XX New ABC1 polypeptide is useful for treating diseases associated with

XX ABC1 biological activity, e.g. Alzheimer's disease, Huntington's

XX disease and cancer -

XX Examples; Page -: 229pp; English.

XX The invention relates to the human ABC1 cholesterol transporter protein  
CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
CC proteins, and plays a crucial role in cholesterol transport, particularly  
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
CC located on chromosome 9q31, and mutations in this gene are associated  
CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
CC are distinguishable in that TD is an autosomal recessive disorder, while  
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
CC cholesterol") in the blood correlate with a high risk of cardiovascular





CC The invention specifically excludes proteins with the exact amino acid  
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
 CC present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
 CC transporter associated with an altered cholesterol level and therefore an  
 CC altered risk of cardiovascular disease.  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the native human ABC1 cDNA shown on pages 157-160.  
 XX  
 SQ Sequence 7864 BP; 2014 A; 1859 C; 2011 G; 1979 T; 1 other;

Query Match 100.0%; Score 501; DB 21; Length 7864;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-148;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAAAGAAACAAACACTGCAGATATCTTCAGGACCTGCAGGAAGAAACATTTGGG 60  
 DB 4537 CACAAAGAAACAAACACTGCAGATATCTTCAGGACCTGCAGGAAGAAACATTTGGG 4596  
 QY 61 ATTATCTGCTGAAGAGCTATGTCAGATCATAGCCAAAGCTTAAAGAACAAAGATCTGGG 120  
 DB 4597 ATTATCTGCTGAAGAGCTATGTCAGATCATAGCCAAAGCTTAAAGAACAAAGATCTGGG 4656  
 QY 121 TGAATGAGTTTATGATGGCGCTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 180  
 DB 4657 TGAATGAGTTTATGATGGCGCTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 4716  
 QY 181 CGAGTCAAGAAGTTAATGATGCTCAACAAATGAAGAAACACCTAAAGCTGGSCAAGG 240  
 DB 4717 CGAGTCAAGAAGTTAATGATGCTCAACAAATGAAGAAACACCTAAAGCTGGSCAAGG 4776  
 QY 241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAGATTTATGACAGACTTGGACACCA 300  
 DB 4777 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAGATTTATGACAGACTTGGACACCA 4836  
 QY 301 GAAATATGTCGAAGTGTTGTTCAATAACAAGGCTGGCGTGCATCAATCACTTTTCCTGA 360  
 DB 4837 GAAATATGTCGAAGTGTTGTTCAATAACAAGGCTGGCGTGCATCAATCACTTTTCCTGA 4896  
 QY 361 ATGTCATCAACAAATGCCATTTCTCGGGCCCAACCTGCAAAAGGGAGAGACCTTAGCCATT 420  
 DB 4897 ATGTCATCAACAAATGCCATTTCTCGGGCCCAACCTGCAAAAGGGAGAGACCTTAGCCATT 4956  
 QY 421 ATGGAATCTACTGTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 480  
 DB 4957 ATGGAATCTACTGTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 5016  
 QY 481 CTCTGATCACCACATCAGTGG 501  
 DB 5017 CTCTGATCACCACATCAGTGG 5037

## RESULT 9

AAAF24680  
 ID AAF24680 standard; DNA; 10442 BP.  
 AC AAF24680;  
 XX  
 XX

DT 20-APR-2001 (first entry)  
 DE Nucleotide sequence of a human ABC1 polypeptide.

Human: adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 291..7076  
 FT /\*tag= a  
 FT /product= "ABC1 polypeptide"  
 FT

XX W0200078972-A2.  
 XX  
 XX 28-DEC-2000.  
 XX  
 XX 16-JUN-2000; 2000WO-US16765.  
 XX  
 XX 18-JUN-1999; 99US-0140264.  
 XX  
 XX 14-SEP-1999; 99US-0153872.  
 XX  
 XX 19-NOV-1999; 99US-0166573.  
 XX  
 XX (CVTH-) CV THERAPEUTICS INC.  
 XX  
 XX Lawn RM, Wade D, Garvin M;  
 XX  
 XX WPI; 2001-137812/14.  
 XX  
 XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
 XX useful for the development of agents for the treatment of heart disease  
 XX and other disorders associated with hypercholesterolemia and  
 XX atherosclerosis.  
 XX  
 XX Disclosure; Page 122-128; 215pp; English.  
 XX  
 XX The present sequence encodes a human adenosine triphosphate (ATP)  
 XX binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
 XX membranes and utilizes ATP hydrolysis to transport a wide variety of  
 XX substrates across the plasma membrane. ABC1 is a pivotal protein in  
 XX the apolipoprotein-mediated mobilisation of intracellular cholesterol  
 XX stores. ABC1 is defective in Tangier disease, a genetic disorder  
 XX characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
 XX localised to chromosome 9q22-9q31. The ABC1 genes and proteins are  
 XX useful for developing pharmaceutical agents for the treatment of heart  
 XX disease and other disorders associated with hypercholesterolemia and  
 XX atherosclerosis. The genes are useful for developing screening assays to  
 XX screen for compounds that regulate the expression of genes associated  
 XX with cholesterol transport. The genes and proteins are also useful for  
 XX are also useful as diagnostic indicators of cardiovascular disease and  
 XX other disorders associated with hypercholesterolemia.  
 XX  
 XX SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 10442;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-148;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAAAGAAACAAACACTGCAGATATCTTCAGGACCTGCAGGAAGAAACATTTGGG 60  
 DB 4750 CACAAAGAAACAAACACTGCAGATATCTTCAGGACCTGCAGGAAGAAACATTTGGG 4809  
 QY 61 ATTATCTGCTGAAGAGCTATGTCAGATCATAGCCAAAGCTTAAAGAACAAAGATCTGGG 120  
 DB 4810 ATTATCTGCTGAAGAGCTATGTCAGATCATAGCCAAAGCTTAAAGAACAAAGATCTGGG 4869  
 QY 121 TGAATGAGTTTATGATGGCGCTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 180  
 DB 4870 TGAATGAGTTTATGATGGCGCTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 4929  
 QY 181 CGAGTCAAGAAGTTAATGATGCTCAACAAATGAAGAAACACCTTAAAGCTGGSCAAGG 240  
 DB 4930 CGAGTCAAGAAGTTAATGATGCTCAACAAATGAAGAAACACCTTAAAGCTGGSCAAGG 4989  
 QY 241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAGATTTATGACAGACTTGGACACCA 300  
 DB 4990 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAGATTTATGACAGACTTGGACACCA 5049  
 QY 301 GAAATATGTCGAAGTGTTGTTCAATAACAAGGCTGGCGTGCATCAATCACTTTTCCTGA 360  
 DB 5050 GAAATATGTCGAAGTGTTGTTCAATAACAAGGCTGGCGTGCATCAATCACTTTTCCTGA 5109  
 QY 361 ATGTCATCAACAAATGCCATTTCTCGGGCCCAACCTGCAAAAGGGAGAGACCTTAGCCATT 420  
 DB 5110 ATGTCATCAACAAATGCCATTTCTCGGGCCCAACCTGCAAAAGGGAGAGACCTTAGCCATT 5169

QY 421 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 480  
|||||  
Db 5170 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 5229  
QY 481 CTCTGATGACCATCAGTGG 501  
|||||  
Db 5230 CTCTGATGACCATCAGTGG 5250

RESULT 10  
AAF24702  
ID AAF24702 standard; DNA; 10442 BP.  
XX AC  
XX AC  
XX DT  
XX DT  
XX 20-APR-2001 (first entry)  
XX DE Nucleotide sequence of a human ABC1 polypeptide.  
XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
XX KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
XX KW atherosclerosis; cholesterol transport; ss.  
XX OS Homo sapiens.  
XX FH Key  
XX FT CDS  
XX FT Location/Qualifiers  
XX FT 291..7076  
XX FT /\*tag= a  
XX FT /product= "ABC1 polypeptide"  
XX PN WO200078971-A2.  
XX PD  
XX PD 28-DEC-2000.  
XX PE 16-JUN-2000; 2000WO-US16591.  
XX PR 18-JUN-1999; 99US-0140264.  
XX PR 14-SEP-1999; 99US-0153872.  
XX PR 19-NOV-1999; 99US-0166573.  
XX PA {CVTH-} CV THERAPEUTICS INC.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Lawn RM, Wade D, Oram JF, Garvin M;  
XX WP; 2001-137811/14.  
XX P-PSDB; AAB31365.  
XX PT Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
XX PT polynucleotides and polypeptides, useful for treatment of heart disease  
XX PT and other disorders associated with hypercholesterolemia and  
XX PT atherosclerosis  
XX PS Claim 3; Page 117-123; 21lpp; English.  
XX CC The present sequence encodes a human adenosine triphosphate (ATP)  
XX CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell  
XX CC membranes and utilises ATP hydrolysis to transport a wide variety of  
XX CC substrates across the plasma membrane. ABC1 is a pivotal protein in  
XX CC the apolipoprotein-mediated mobilisation of intracellular cholesterol  
XX CC stores. ABC1 is defective in Tangier disease, a genetic disorder  
XX CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is  
XX CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are  
XX CC useful for developing pharmaceutical agents for the treatment of heart  
XX CC disease and other disorders associated with hypercholesterolemia and  
XX CC atherosclerosis. The genes are useful for developing screening assays to  
XX CC screen for compounds that regulate the expression of genes associated  
XX CC with cholesterol transport. The genes and proteins are also useful for  
XX CC are also useful as diagnostic indicators of cardiovascular disease and  
XX CC other disorders associated with hypercholesterolemia.

SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;  
Query Match 100.0%; Score 501; DB 22; Length 10442;  
Best Local Similarity 100.0%; Pred. No. 8.2e-148;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACAAAGAAACAAACACATCGATATCCCTTCAGGACCTCAGAGGAAGAAACATTTTCGG 60  
|||||  
Db 4750 CACAAAGAAACAAACACATCGATATCCCTTCAGGACCTCAGAGGAAGAAACATTTTCGG 4809  
QY 61 ATTATCTGTTGAAGACGTATGTGCAGATCATAGCCAAAGCTTAAAGAACAAAGATTCGGG 120  
|||||  
Db 4810 ATTATCTGTTGAAGACGTATGTGCAGATCATAGCCAAAGCTTAAAGAACAAAGATTCGGG 4869  
QY 121 TGAATGAGTTTAGTATGGCGCTTTCCCTGGGTGCTAGTAATCAAGCACTTCTCTC 180  
|||||  
Db 4870 TGAATGAGTTTAGTATGGCGCTTTCCCTGGGTGCTAGTAATCAAGCACTTCTCTC 4929  
QY 181 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGTGCCCAAGG 240  
|||||  
Db 4930 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTAAAGTGCCCAAGG 4989  
QY 241 ACAGTTCGAGATCGATTTCTCAACAGCTTGGGAGATTTTATGACAGGACTGGACACCA 300  
|||||  
Db 4990 ACAGTTCGAGATCGATTTCTCAACAGCTTGGGAGATTTTATGACAGGACTGGACACCA 5049  
QY 301 GAATAATGTCAGGTGTGGTTCAATAACAAGGGTGGCATGCAATCAGCTCTTCTCTGA 360  
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Db 5050 GAATAATGTCAGGTGTGGTTCAATAACAAGGGTGGCATGCAATCAGCTCTTCTCTGA 5109  
QY 361 ATGTCATCAACAAATGCCATTCCTCGGGCCACCTCCAAAGAGGAGAACCTTAGCCATT 420  
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Db 5110 ATGTCATCAACAAATGCCATTCCTCGGGCCACCTCCAAAGAGGAGAACCTTAGCCATT 5169  
QY 421 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 480  
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Db 5170 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGCAGCTCTCAGAGGTGG 5229  
QY 481 CTCTGATGACCATCAGTGG 501  
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Db 5230 CTCTGATGACCATCAGTGG 5250

RESULT 11  
AAF24685  
ID AAF24685 standard; DNA; 10474 BP.  
XX AC AAF24685;  
XX AC AAF24685;  
XX DT 20-APR-2001 (first entry)  
XX DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
XX KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
XX KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
XX KW atherosclerosis; cholesterol transport; ss.  
XX OS Homo sapiens.  
XX FH Key  
XX FT CDS  
XX FT Location/Qualifiers  
XX FT 323..7108  
XX FT /\*tag= a  
XX FT /product= "defective ABC1 polypeptide"  
XX PN WO200078972-A2.  
XX PD  
XX PD 28-DEC-2000.  
XX PE 16-JUN-2000; 2000WO-US16765.  
XX PR 18-JUN-1999; 99US-0140264.  
XX PR 14-SEP-1999; 99US-0153872.



[illegible]

RESULT 13

RESUL IS  
AAE24707  
ID AAE24707 standard; DNA; 10474 BP.

AC AAF24707;

20-APR-2001 (first entry)

XX  
DE Nucleotide sequence of ABC1 polypeptide from Tanqier disease patient.

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.

YY Homo sapiens.

| XX | Key | Location/Qualifiers |
|----|-----|---------------------|
| FH | CDS | 323.7108            |
| FT |     |                     |

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FF      /*tag= a
FF      /*product=
FF      /*defective ABC1 polymer iden"

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XX  
DN  
W0300079971-23

XX 0000-0000

XX  
10-11-2000.

XX-

PR 14-SEP-1999; 99US-0153872.

XX

PA (UNIW ) UNIV WASHINGTON.

PI Lawn RM, Wade D, Oram JF, Garvin M;

DR WPI; 2001-137811/14.

NR FDD, FDD, FDD

XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
PT polynucleotides and polypeptides, useful for treatment of heart disease  
PT and other disorders associated with hypercholesterolemia and  
PT atherosclerosis -  
XX  
XX Claim 27; Page 144-150; 211pp; English.  
PS  
XX The present sequence encodes a human adenosine triphosphate (ATP)  
CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
CC ATP hydrolysis to transport a wide variety of substrates across the  
CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
CC Tangier disease, a genetic disorder characterised by abnormal  
CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
CC 9q22-qq31. The ABC1 genes and proteins are useful for developing  
CC pharmaceutical agents for the treatment of heart disease and other  
CC disorders associated with hypercholesterolemia and atherosclerosis. The  
CC genes are useful for developing screening assays to screen for compounds  
CC that regulate the expression of genes associated with cholesterol  
CC transport. The genes and proteins are also useful for are also useful  
CC as diagnostic indicators of cardiovascular disease and other disorders  
CC associated with hypercholesterolemia.  
XX  
XX Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other

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Query Match      100.0%; Score 501; DB 22; Length 10474;
Best Local Similarity 100.0%; Pred. No. 8.2e-148;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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| Qy | 181  | CGAGTCAAGAAGTTTAATGATGCCATCAAAACAATGAAGAAACACCTAAAGCTGGCCAAAG     | 240  |
| Db | 4962 | CGAGTCAAGAAGTTTAATGATGCCATCAAAACAATGAAGAAACACCTAAAGCTGGCCAAAG     | 5021 |
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| Db | 5022 | ACAGTTCTGCAGATCGAATTTCTAACAGCTTGGGAAGATTTATGACGAGATGNCACCA        | 5081 |
| Qy | 301  | GAATTAATGTCAAAGTGTGGTTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCCTGA    | 360  |
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| Qy | 361  | ATGTCATCAACAATGCCAATTTCTCGGGGCAACCTCCAAAAGGGAGAGAACCTTAGCCATT     | 420  |
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| Qy | 421  | ATGGAAATTAATCTGCTTTTCAATCATCCCTGAAATCTCACCAAAGCAGCAGCTCTCAGAGGTGG | 480  |
| Db | 5202 | ATGGAAATTAATCTGCTTTTCAATCATCCCTGAAATCTCACCAAAGCAGCAGCTCTCAGAGGTGG | 5261 |
| Qy | 481  | CTCTGATGAACCATCATAGTGG  | 501  |
| Db | 5262 | CTCTGATGAACCATCATAGTGG  | 5282 |

## RESULT 14

RESULTS  
AAF24708  
ID AAF24708 standard; DNA; 10474 BP.  
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AC AAF24708;

XX XX 20-APR-2001 (first entry)  
 XX XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.  
 DE XX  
 XX XX Human: adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.  
 XX OS Homo sapiens.  
 XX XX  
 XX XX Location/Qualifiers  
 FH Key 323..7108  
 FT CDS /tag= a  
 FT /product= "defective ABC1 polypeptide"  
 XX XX  
 XX PN WO200078971-A2.  
 XX XX 28-DEC-2000.  
 XX XX 16-JUN-2000; 2000WO-US16591.  
 XX XX 18-JUN-1999; 99US-0140264.  
 PR 14-SEP-1999; 99US-0153672.  
 PR 19-NOV-1999; 99US-0166573.  
 XX XX (CVTR-) CV THERAPEUTICS INC.  
 XX XX (UNIW ) UNIV WASHINGTON.  
 XX XX  
 XX XX Lawn RM, Wade D, Oram JF, Garvin M;  
 XX WPI; 2001-137811/14.  
 DR P-PSDB; AAB31367.  
 XX XX  
 XX XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
 PT polynucleotides and polypeptides, useful for treatment of heart disease  
 PT and other disorders associated with hypercholesterolemia and  
 PT atherosclerosis -  
 XX XX  
 XX XX Claim 30; Page 165-172; 21pp; English.  
 XX XX  
 XX XX The present sequence encodes a human adenosine triphosphate (ATP)  
 CC binding cassette protein (ABC) 1 polypeptide, and is isolated from  
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilises  
 CC ATP hydrolysis to transport a wide variety of substrates across the  
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in  
 CC Tangier disease, a genetic disorder characterised by abnormal  
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing  
 CC pharmaceutical agents for the treatment of heart disease and other  
 CC disorders associated with hypercholesterolemia and atherosclerosis. The  
 CC genes are useful for developing screening assays to screen for compounds  
 CC that regulate the expression of genes associated with cholesterol  
 CC transport. The genes and proteins are also useful for also useful  
 CC as diagnostic indicators of cardiovascular disease and other disorders  
 CC associated with hypercholesterolemia.  
 XX XX  
 XX XX Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;  
 SQ  
 Query Match 100.0%; Score 501; DB 22; Length 10474;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-148;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CACCAAGAAACAAACACTGCAGATATCTTCAGGACCTGACAGGAAGAAACATTTCCG 60  
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QY 121 TGAATGAGTTAGTATGGGGCTTTTCCTGGTCTCAGTAACTCAAGCACTTCTC 180  
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 Db ATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCTAGCCATT 5201  
 QY 421 ATGGAATTACTGCTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 480  
 Db ATGGAATTACTGCTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 5261  
 QY 481 CTCTGATGACCATCAGTGG 501  
 Db CTCTGATGACCATCAGTGG 5282  
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 AA294734  
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 XX AC AA294734;  
 XX DT 01-AUG-2000 (first entry)  
 XX DE Human ATP binding cassette ABCA1 (ABCI) cDNA.  
 XX KW ABCA1; ABC1; ATP binding cassette; human; cholesterol;  
 KW interleukin-1 beta; transporter; inflammation; septic shock;  
 KW rheumatoid arthritis; Tangier disease; hypertriglyceridemia;  
 KW splenomegaly; atherosclerosis; lipid disorder; dyslipidemia;  
 KW psoriasis; lupus erythematosus; diagnosis; gene therapy;  
 KW chromosome 9q22-31; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 121..6726  
 FT /\*tag= a  
 XX PN WO200018912-A2.  
 XX PD 06-APR-2000.  
 XX PF 21-SEP-1999; 99WO-EP06991.  
 XX PR 25-SEP-1998; 98US-0101706.  
 XX PA (FARB ) BAYER AG.  
 XX PI Schmitz G, Klucken J;  
 XX DR WPI; 2000-293151/25.  
 XX P-PSDB; AAY79380.  
 XX XX Adenosine triphosphate binding proteins useful for identifying agents  
 PT for treating atherosclerosis and other inflammatory disorders -  
 XX XX Claim 9; Page 90-93; 154pp; English.  
 XX XX The present sequence is that of human cDNA encoding ATP binding  
 CC

cassette protein ABC1 (ABC1, see AAY79380), the human homologue of mouse ABC1. The cDNA was identified using a differential display method in which monocytes from peripheral blood were subjected to macrophage differentiation and cholesterol loading with acetylated low density lipoproteins and subsequent deloading with high density lipoprotein (HDL3) to identify cholesterol sensitive genes. The ABCA1 gene maps to human chromosome 9q22-31. Dysregulated ABCA1 is the gene locus involved in the HDL deficiency syndrome Tangier disease, associated with hypertriglyceridemia and splenomegaly. ABCA1 is also a transporter for interleukin-1 beta, making the gene a candidate for treatment of inflammatory diseases such as rheumatoid arthritis and septic shock. The invention also provides other cholesterol-sensitive ABC genes (see AA294735-63) that can be used for diagnostic and therapeutic applications, and for biochemical or cell-based assays to screen for pharmacologically active compounds useful for the treatment of lipid disorders, atherosclerosis or other inflammatory diseases such as psoriasis and lupus erythematosus.

XX Sequence 6880 BP; 1760 A; 1656 C; 1783 G; 1681 T; 0 other;

Query Match 99.4%; Score 497.8; DB 21; Length 6880;  
Best Local Similarity 99.6%; Pred. No. 6.9e-147;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 4820 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCAGCAGAGCTCTCAGAGGTGG 4879  
QY 481 CTCGTATGACCATCAGTGG 501  
DB 4880 CTCGTATGACCATCAGTGG 4900

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.777 Seconds  
(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
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| C 3        | 31.6  | 6.3         | 5679   | 1  | US-08-201-697-1    |
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| C 5        | 30.8  | 6.1         | 1951   | 2  | US-08-478-435-112  |
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| C 7        | 30.8  | 6.1         | 1951   | 2  | US-08-478-373-112  |
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| C 11       | 30.8  | 6.1         | 1951   | 4  | US-08-637-654-112  |
| C 12       | 30.8  | 6.1         | 1951   | 4  | US-08-649-518-112  |
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| C 14       | 30.6  | 6.1         | 2834   | 1  | US-08-276-151-8    |
| C 15       | 30.6  | 6.1         | 3073   | 1  | US-07-688-352C-31  |
| C 16       | 30.6  | 6.1         | 3073   | 2  | US-08-474-379C-31  |
| C 17       | 30.6  | 6.1         | 3073   | 3  | US-09-146-249A-31  |
| C 18       | 30.6  | 6.1         | 3073   | 3  | US-08-206-188B-31  |
| C 19       | 30.6  | 6.1         | 3073   | 5  | PCT-US91-02714-30  |
| C 20       | 30.6  | 6.1         | 35100  | 1  | US-08-306-691B-19  |
| C 21       | 30.6  | 6.1         | 35100  | 5  | PCT-US93-06251-19  |
| C 22       | 30.4  | 6.1         | 2166   | 4  | US-09-134-078-5    |
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| 28   | 29.2 | 5.8 | 1866  | 1 | US-08-658-578-1   | Sequence 1, Appli  |
| 29   | 29.2 | 5.8 | 1866  | 3 | US-08-846-111D-1  | Sequence 1, Appli  |
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| 40   | 29.2 | 5.8 | 5099  | 4 | US-08-649-518-4   | Sequence 4, Appli  |
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| 42   | 29.2 | 5.8 | 40352 | 4 | US-09-443-077-15  | Sequence 15, Appli |
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| C 44 | 29   | 5.8 | 2176  | 3 | US-09-090-808-3   | Sequence 3, Appli  |
| C 45 | 29   | 5.8 | 2176  | 4 | US-09-447-453-3   | Sequence 3, Appli  |

ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-F1s  
US-08-232-463-14

Query Match 7.9%; Score 39.4; DB 1; Length 7218;

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Best Local Similarity 5.7%; Pred. No. 0.012;
Matches 22; Conservative 196; Mismatches 167; Indels 0; Gaps 0;

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    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Qy 184 GTCAGAGCTTAATGATCCATCAACAAATGAAGAACACCTAAGCTGCCAAGGACA 243
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1221 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 244 GTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATTTATGACAGACTGGACACAGAA 303
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1161 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1102
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 304 ATAATGTCAGAGTGTGTTCAATAACAGGCTGGCATGCAATCAGCTTCTTCCTGA 363
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1101 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1042
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 364 TCATCAACAATGCATCTCCGGC 388
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1041 CAAGCTCGGAATTAATCTGTGAGC 1017
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; FILE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103806
; OTHER INFORMATION: 5-131-395 : polymorphic base A or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106940
; OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108106
; OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108149
; OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108308
; OTHER INFORMATION: 5-135-357 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108471
; OTHER INFORMATION: 5-136-174 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134134
; OTHER INFORMATION: 5-140-120 : polymorphic base C or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134362
; OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
; FEATURE:
; NAME/KEY: allele
; LOCATION: 134374
; OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
; FEATURE:
; NAME/KEY: allele
; LOCATION: 146328
; OTHER INFORMATION: 5-143-84 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 146345
; OTHER INFORMATION: 5-143-101 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 150329
; OTHER INFORMATION: 5-145-24 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 160031
; OTHER INFORMATION: 5-148-352 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 7271..72817
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
; FEATURE:
; NAME/KEY: allele
; LOCATION: 7271..72817
; OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
; FEATURE:

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; NAME/KEY: allele
; LOCATION: 8050..8096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
; FEATURE:
; NAME/KEY: allele
; LOCATION: 8050..8096
; OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90819..90865
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90819..90865
; OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93690..93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93690..93736
; OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97099..97145
; OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97099..97145
; OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97130..97177
; OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97130..97177
; OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99075..99121
; OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99075..99121
; OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99094..99140
; OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103783..103828
; OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
; FEATURE:
; NAME/KEY: allele
; LOCATION: 106918..106966
; OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
; FEATURE:
; NAME/KEY: allele

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; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
; FEATURE:
Query Match 6.6%; Score 33.2; DB 4; Length 162450;
Best Local Similarity 51.3%; Pred. No. 7.2;
Matches 77; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 235 CCAAGGACAGTTCGACATCGATTTCTCAACAGCTTGGGAAGATTATGACAGGACTGG 294
Db 41002 CAAGAAAGAGAACTAGAGAGACACCCAAACTCGAGGGAGTTGTAGTAAACAAGCAG 40943
QY 295 ACACGAGAAATAATGTCAGAGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTTT 354
Db 40942 AAGACAAAGGAATTCAGGTGAGGCTACAGGGCAAGAACAGTCTCATTGTGTCTG 40883
QY 355 TCCTGAATGTCATCAACAATGCCATTCTCC 384
Db 40882 TCTTGAATGTACCAAGAACTACCAGTGTTC 40853

RESULT 3
US-08-201-697-1
; Sequence 1, Application US/08201697
; Patent No. 5705623
; GENERAL INFORMATION:
; APPLICANT: Wiggins, Roger C.
; APPLICANT: Thomas, Feedikayil E.
; TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
; TITLE OF INVENTION: 1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201.697
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UM 9783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5679 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:

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/ NAME/KEY: CDS
/ LOCATION: 180...3740
US-08-201-697-1

Query Match      6.3%; Score 31.6; DB 1; Length 5679;
Best Local Similarity 58.5%; Pred. No. 3.8;
Matches 55; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 172 CACTTCTCCGAGTCAAGAAGTTAATGATGCCATCAAAACAAATGAAGAAACACCTAAAGC 231
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2668 CACTTCTAATGGTCTGCTGTGTACTCTCATCTCTTAGGAGAAACATCTGCAGA 2727

QY 232 TGGCCAGACAGATCTTCGACGATCGATTTCTCAA 265
      ||||| |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2728 TGGCTAGGAGTGTGGAGCAGGAACATTGTGCAA 2761

RESULT 4
US-08-487-890A-112
; Sequence 112, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08487,890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1890
US-08-487-890A-112

Query Match      6.1%; Score 30.8; DB 1; Length 1951;
Best Local Similarity 57.1%; Pred. No. 3.8;

Best Local Similarity 57.1%; Pred. No. 3.8;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 193 AGTCAAGAAGTTAATGATGCCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAGGAC 242
      ||||| |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 790 AATCTAGAAGCTGATGTGTATAGCAACCGATTACAGAGTTAAAGTAAAGCCCAACCAAGAG 849

QY 243 AGTTCTGCAGATCGATTTCCTCAACAGAGCTTGGGAAGATT 280
      ||||| |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 850 TCTTCTGAAGAACAATCCCTTTTACCAGCGAGGGAACATT 887

RESULT 5
US-08-478-435-112
; Sequence 112, Application US/08478435
; Patent No. 592323
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1890
US-08-478-435-112

Query Match      6.1%; Score 30.8; DB 2; Length 1951;
Best Local Similarity 57.1%; Pred. No. 3.8;
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; Sequence 112, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,577A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1890
; US-08-483-577A-112

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Query Match          6.1%; Score 30.8; DB 3; Length 1951;
Best Local Similarity 57.1%; Pred. No. 3.8;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 183 AGTCAGAGAGTTAATGATGCCATCAACAAATGAAGAACACCTTAAGCTGGCCCAAGGAC 242
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 790 ATCTTGAAGCTGATGTTATAGCAACCGATTTCAGAGGTAAAGTAAAGCCACCAAGAG 849

QY 243 AGTTTGCAGATCGATTTCTCAACAGCTTGGGAAGATT 280
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 850 TCCTTCGAAGAACATCCCTTTACCGAGGAGGGAACATT 887

RESULT 10
US-08-897-438-112
; Sequence 112, Application US/08897438
; Patent No. 6262016

```

GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M  
APPLICANT: Harkness, Robin E  
APPLICANT: Schryvers, Anthony B  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Murdin, Andrew D  
APPLICANT: Klein, Michel H  
TITLE OF INVENTION: Transferrin Receptor Genes  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/897,438  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,577  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,483  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/175,116  
FILING DATE: 29-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/148,968  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-720  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1951 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1890  
US-08-897-438-112

Query Match 6.1%; Score 30.8; DB 4; Length 1951;  
Best Local Similarity 57.1%; Pred. No. 3.8;  
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 183 AGTCAAGACGTATGATGCGATCAACAACATGAGAACACCTTAAGCTGGCCCAAGGAC 242  
Db 790 AATCTGAAGAGCTGATGTATAGCAACCGATTACAGAGTAAAGTAAAGCCAAACCAAGAG 849

Qy 243 AGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATT 280  
Db 850 TCTTCTGAAGAACATCCCTTTACCAGGAGGGAACAATT 887

RESULT 11  
US-08-637-654-112  
; Sequence 112, Application US/08637654

Patent No. 6358727  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena M  
APPLICANT: Harkness, Robin E  
APPLICANT: Schryvers, Anthony B  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping  
APPLICANT: Murdin, Andrew D  
APPLICANT: Klein, Michel H  
TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sim & McBurney  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/637,654  
FILING DATE: 05-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA94/00616  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-595  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1951 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1890  
US-08-637-654-112

Query Match 6.1%; Score 30.8; DB 4; Length 1951;  
Best Local Similarity 57.1%; Pred. No. 3.8;  
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 183 AGTCAAGACGTATGATGCGATCAACAACATGAGAACACCTTAAGCTGGCCCAAGGAC 242  
Db 790 AATCTGAAGAGCTGATGTATAGCAACCGATTACAGAGTAAAGTAAAGCCAAACCAAGAG 849

Qy 243 AGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATT 280  
Db 850 TCTTCTGAAGAACATCCCTTTACCAGGAGGGAACAATT 887

RESULT 12  
US-08-649-518-112  
; Sequence 112, Application US/08649518  
GENERAL INFORMATION:  
APPLICANT: Loosmore, Sheena  
APPLICANT: Harkness, Robin  
APPLICANT: Schryvers, Anthony  
APPLICANT: Chong, Pele  
APPLICANT: Gray-Owen, Scott  
APPLICANT: Yang, Yan-Ping

```

1  APPLICANT: Murdin, Andrew
2  APPLICANT: Klein, Michel
3  TITLE OF INVENTION: Transferrin Receptor Genes
4  NUMBER OF SEQUENCES: 160
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Sim & McBurney
7  STREET: 6th Floor, 330 University Avenue
8  CITY: Toronto
9  STATE: Ontario
10 COUNTRY: Canada
11 ZIP: M5G 1R7
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patentin Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/649,518
20 FILING DATE: 17-MAY-1996
21 CLASSIFICATION: 536
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/337,483
24 FILING DATE: 08-NOV-1994
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/483,577
27 FILING DATE: 07-JUN-1995
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/175,116
30 FILING DATE: 29-DEC-1993
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/148,968
33 FILING DATE: 08-NOV-1993
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Stewart, Michael I
36 REGISTRATION NUMBER: 24,973
37 REFERENCE/DOCKET NUMBER: 1038-608
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: (416) 595-1155
40 TELEFAX: (416) 595-1163
41 INFORMATION FOR SEQ ID NO: 112:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 1951 base pairs
44 TYPE: nucleic acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 FEATURE:
48 NAME: CDS
49 LOCATION: 1..1890
50 US-08-649-518-112

```

[illegible]

RESULT 13  
US-09-157-177-104  
; Sequence 104, Application US/09157177  
; Patent No. 6090558  
; GENERAL INFORMATION:  
; APPLICANT: Butler, John M.  
; APPLICANT: Li, Jia  
; APPLICANT: Monforte, Joseph A.  
; APPLICANT: Becker, Christopher H.  
; TITLE OF INVENTION: DNA TYPING BY MASS SPECTROMETRY

```

; TITLE OF INVENTION: REPEAT MARKERS
; FILE REFERENCE: GETR:017/GETR017P
; CURRENT APPLICATION NUMBER: US/09/157,177
; CURRENT FILING DATE: 1998-09-18
; EARLIER APPLICATION NUMBER: 60/059,415
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-157-177-104

Query Match      6.1%   Score 30.6;   DB 3;   Length 315;
Best Local Similarity 60.08; Pred. No. 1.6;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps

QY  240  GACAGCTTCTGCAGATCGCATTTCTTCAACAGAGCTTCGGGAAGATTATCACAGAGCTTGGACACC 192
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db    133  GATAGATAGATAGATAGATAGATAGATAGATAGATAGGAAGTACTTAGACACAGGCTCTGCACCA 192

QY  300  AGAAATANTGTCAAGGTGTGGTTCA 324
      ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||  ||||
Db    193  GGAAATGCTGTCCAAGTGTGCACCA 217

RESULT 14
US-08-276-151-8/c
; Sequence 8, Application Us/08276151

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RESULT 14  
 US-08-276-151-8/c  
 ; Sequence 8, Application US/08276151  
 ; Patent No. 5597719  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Freed, Ellen  
 ; APPLICANT: Ruggieri, Rosamaria  
 ; TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooley Godward et al.  
 ; STREET: Five Palo Alto Square  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/276,151  
 ; FILING DATE: 14-JUL-1994  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Torchia, Ph.D., Timothy E  
 ; REGISTRATION NUMBER: 36,700  
 ; REFERENCE/DOCKET NUMBER: ONYX-005/0005  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 843-5461  
 ; TELEFAX: (415) 857-0663  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2834 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; HYPOTHEetical: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 85..822  
 ; US-08-276-151-8



QY 62 TTATCTGGTGAAGACGCTATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTG 118  
 DB 2287 ATCAAAATTGAAGGCGAGCTATAAGAGTATCAAGAAATTTCTTAAAAACCAAAAAGTG 2231

Search completed: April 3, 2003, 14:23:09  
 Job time : 106.777 secs

Query Match 6.1%; Score 30.6; DB 1; Length 2834;  
 Best Local Similarity 53.8%; Pred. No. 5.4;  
 Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 ACAAGAAACAAACACTGCGAGATATCTTCAGGACCTGACAGGAGAAACATTTTCGGA 61  
 DB 2327 AGACAGAGGCTAAACACAGGAGGTAATCTTGTGCACCTGACAAATAGAAAGATAAAGG 2268  
 QY 62 TTATCTGGTGAAGACGCTATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTG 118  
 DB 2267 ATCAAAATTGAAGGCGAGCTATAAGAGTATCAAGAAATTTCTTAAAAACCAAAAAGTG 2211

RESULT 15

US-07-688-352C-31/c  
 ; Sequence 31, Application US/07688352C  
 ; Patent No. 5527896  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wigler, Michael H.  
 ; APPLICANT: Colicelli, John J.  
 ; TITLE OF INVENTION: Cloning by Complementation and Related  
 ; TITLE OF INVENTION: Processes  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
 ; ADDRESSEE: Bicknell  
 ; STREET: Street  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60603

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/688,352C  
 FILING DATE: 19910419  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/511,715  
 FILING DATE: 20-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Borun, Michael F.  
 REGISTRATION NUMBER: 25447  
 REFERENCE/DOCKET NUMBER: 27805/30197  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (312) 346-5750  
 TELEFAX: (312) 984-9740  
 TELEX: 25-3856  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3073 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3..1111  
 US-07-688-352C-31

Query Match 6.1%; Score 30.6; DB 1; Length 3073;  
 Best Local Similarity 53.8%; Pred. No. 5.7;  
 Matches 63; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 2 ACAAGAAACAAACACTGCGAGATATCTTCAGGACCTGACAGGAGAAACATTTTCGGA 61  
 DB 2347 AGACAGAGGCTAAACACAGGAGGTAATCTTGTGCACCTGACAAATAGAAAGATAAAGG 2288

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 16:38:15 ; Search time 31.6923 Seconds  
(without alignments)  
13866.500 Million cell updates/sec

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Perfect score: 501  
Sequence: 1 cacaaagaaacacacact.....tctgatgaccacatcagtgg 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published\_Applications\_NA:\*
- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
  - 2: /cgn2\_6/ptodata/2/pubpna/PTI\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
  - 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
  - 6: /cgn2\_6/ptodata/2/pubpna/PTUS\_PUBCOMB.seq:\*
  - 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
  - 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
  - 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
  - 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
  - 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
  - 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
  - 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description       |
|------------|-------|---------------|--------|----|-------------------|
| 1          | 497.8 | 99.4          | 8925   | 9  | US-09-802-640-27  |
| 2          | 497.8 | 99.4          | 9741   | 10 | US-09-846-456-10  |
| 3          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-92  |
| 4          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-93  |
| 5          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-94  |
| 6          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-95  |
| 7          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-96  |
| 8          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-97  |
| 9          | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-98  |
| 10         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-99  |
| 11         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-100 |
| 12         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-101 |
| 13         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-102 |
| 14         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-103 |
| 15         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-104 |
| 16         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-105 |
| 17         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-106 |
| 18         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-107 |
| 19         | 497.8 | 99.4          | 9870   | 9  | US-09-984-827-108 |

ALIGNMENTS

RESULT 1  
US-09-802-640-27  
; Sequence 27, Application US/09802640  
; Publication No. US20030036057A1  
; GENERAL INFORMATION:  
; APPLICANT: Braun, Andreas  
; APPLICANT: Bonsal Aruna  
; APPLICANT: Klevn Patrick  
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE  
; FILE REFERENCE: 24736-2048  
; CURRENT APPLICATION NUMBER: US/09/802.640  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 8925  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (5020)...(6162)  
; OTHER INFORMATION: Nucleotide encoding ATP-binding cassette (ABCL)  
; OTHER INFORMATION: n= a or g or c or t  
US-09-802-640-27

|                       |       |   |           |            |    |        |       |
|-----------------------|-------|---|-----------|------------|----|--------|-------|
| Query Match           | 99.4% | Score   | 497.8;    | DB         | 9; | Length | 8925; |
| Best Local Similarity | 99.6% | Pred. No.   | 4.6e-153; |            |    |        |       |
| Matches               | 499;  | Conservative  | 2;        | Mismatches | 0; | Indels | 0;    |
| Gaps                  | 0;    |   |           |            |    |        |       |
| QY                    | 1     | CACAAAGAAACAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAACATTTGG    | 60        |            |    |        |       |
|                       |       |   |           |            |    |        |       |
| DB                    | 4399  | CACAAAGAAACAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAACATTTGG    | 4458      |            |    |        |       |
|                       |       |   |           |            |    |        |       |
| QY                    | 61    | ATTATCTGTTGAAGACGTATGTCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG | 120       |            |    |        |       |
|                       |       |   |           |            |    |        |       |
| DB                    | 4459  | ATTATCTGTTGAAGACGTATGTCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG | 4518      |            |    |        |       |
|                       |       |   |           |            |    |        |       |
| QY                    | 121   | TGAATGAGTTAGGTATCGCGCTTTCCCTGGGGTGTGAGTAATCTCAAGCACTTCCTC | 180       |            |    |        |       |
|                       |       |   |           |            |    |        |       |
| DB                    | 4519  | TGAATGAGTTAGGTATCGCGCTTTCCCTGGGGTGTGAGTAATCTCAAGCACTTCCTC | 4578      |            |    |        |       |
|                       |       |   |           |            |    |        |       |

QY 181 CGAGTCAGAAGTTAATGATGCGCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAAAGG 240  
Db 4579 CGAGTCAGAAGTTAATGATGCGCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAAAGG 4638  
QY 241 ACAGTCTCCAGATCGATTTCACACAGCTTGGGAAGATTATGACAGAGCTGGACACCA 300  
Db 4639 ACAGTCTCCAGATCGATTTCACACAGCTTGGGAAGATTATGACAGAGCTGGACACCA 4698  
QY 301 GAAATTAATGTCGAAGTGTGTTCAATAACAAGGGCTGGCATGCAATCAAGCTCTTTCTTGA 360  
Db 4699 AAAAAAATGTCGAAGTGTGTTCAATAACAAGGGCTGGCATGCAATCAAGCTCTTTCTTGA 4759  
QY 361 ATGTGATCAACAAATGCCATTCTCGGGGCAACCTGCAAAAAGGAGAGAACCTTAGCCATT 420  
Db 4759 ATGTGATCAACAAATGCCATTCTCGGGGCAACCTGCAAAAAGGAGAGAACCTTAGCCATT 4818  
QY 421 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCACAGCAGCAGCTCTCAGAGTGG 480  
Db 4819 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCACAGCAGCAGCTCTCAGAGTGG 4878  
QY 481 CTCTGATGACCAATCATGTTGG 501  
Db 4879 CTCTGATGACCAATCATGTTGG 4899

## RESULT 2

US-09-846-456-10  
; Sequence 10, Application US/09846456  
; Patent No. US20020146792A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosier, Marie  
; APPLICANT: Prades, Catherine  
; APPLICANT: Lemoine, Cendrine  
; APPLICANT: Naudin, Laurence  
; APPLICANT: Deneffe, Patrice  
; APPLICANT: Duverger, Nicolas  
; APPLICANT: Brewer, Bryan  
; APPLICANT: Remaley, Alan  
; APPLICANT: Fofa, Silvia  
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying it  
; TITLE OF INVENTION: Activity and Therapeutic Uses  
; FILE REFERENCE: 3806.0505  
; CURRENT APPLICATION NUMBER: US/09/846.456  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,280  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 9741  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: "n" is chosen from g, a, t and c  
US-09-846-456-10

Query Match 99.4%; Score 497.8; DB 10; Length 9741;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 60  
Db 4644 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 4703  
QY 61 ATTATCTGGTGAAGACGATGTCGAGATCATAGCCAAAGCTTAAAGAAACAGATCTGGG 120  
Db 4704 ATTATCTGGTGAAGACGATGTCGAGATCATAGCCAAAGCTTAAAGAAACAGATCTGGG 4763  
QY 121 TGAATGAGTTTATGATGGCGGCTTTTCCCTGGGTGTCAGTAATACCTCAAGCAGCTTCCCTC 180  
Db 4764 TGAATGAGTTTATGATGGCGGCTTTTCCCTGGGTGTCAGTAATACCTCAAGCAGCTTCCCTC 4823

QY 181 CGACTCAAGAGTTAATGATGCGCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAAAGG 240  
Db 4824 CGACTCAAGAGTTAATGATGCGCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAAAGG 4883  
QY 241 ACAGTCTCCAGATCGATTTCACACAGCTTGGGAAGATTATGACAGAGCTGGACACCA 300  
Db 4884 ACAGTCTCCAGATCGATTTCACACAGCTTGGGAAGATTATGACAGAGCTGGACACCA 4943  
QY 301 GAAATTAATGTCGAAGTGTGTTCAATAACAAGGGCTGGCATGCAATCAAGCTCTTTCTTGA 360  
Db 4944 GAAATTAATGTCGAAGTGTGTTCAATAACAAGGGCTGGCATGCAATCAAGCTCTTTCTTGA 5003  
QY 361 ATGTGATCAACAAATGCCATTCTCGGGGCAACCTGCAAAAAGGAGAGAACCTTAGCCATT 420  
Db 5004 ATGTGATCAACAAATGCCATTCTCGGGGCAACCTGCAAAAAGGAGAGAACCTTAGCCATT 5063  
QY 421 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCACAGCAGCAGCTCTCAGAGTGG 480  
Db 5064 ATGGAATTACTGCTTTCAATCATCCCTGAATCTCACCACAGCAGCAGCTCTCAGAGTGG 5123  
QY 481 CTCTGATGACCAATCATGTTGG 501  
Db 5124 CTCTGATGACCAATCATGTTGG 5144

## RESULT 3

US-09-984-827-92  
; Sequence 92, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFFE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUINE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABC1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-92

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 60  
Db 4773 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 4832  
QY 61 ATTATCTGGTGAAGACGATGTCGAGATCATAGCCAAAGCTTAAAGAAACAGATCTGGG 120  
Db 4833 ATTATCTGGTGAAGACGATGTCGAGATCATAGCCAAAGCTTAAAGAAACAGATCTGGG 4892  
QY 121 TGAATGAGTTTATGATGGCGGCTTTTCCCTGGGTGTCAGTAATACCTCAAGCAGCTTCCCTC 180  
Db 4893 TGAATGAGTTTATGATGGCGGCTTTTCCCTGGGTGTCAGTAATACCTCAAGCAGCTTCCCTC 4952  
QY 181 CGAGTCAAGAAGTTAATGATGCGCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAAAGG 240

Db 4953 CGAGTCAGAAAGTTAATGATGCCACCAACAAATGAAGAAACACCTTAAGCTGCCAAGG 5012  
QY 241 ACAGTTCTCGACATCGATTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
Db 5013 ACAGTTCTCGACATCGATTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
QY 301 GAAATAATCTCAAGGTGTGGTTCAATAACAAGGGTGGCATGCAATCAGCTCTTCCCTGA 360  
Db 5073 GAAATAATCTCAAGGTGTGGTTCAATAACAAGGGTGGCATGCAATCAGCTCTTCCCTGA 5132  
QY 361 ATGTCAATCAACATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 420  
Db 5133 ATGTCAATCAACATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 5192  
QY 421 ATGGAATTAATCTGTTTCAATCATFCCCTGAAATCTCACCAGGAGGCTCTCAGAGGTGG 480  
Db 5193 ATGGAATTAATCTGTTTCAATCATFCCCTGAAATCTCACCAGGAGGCTCTCAGAGGTGG 5252  
QY 481 CTCTGATGACCACATCAGTGG 501  
Db 5253 CTCCGATGACCACATCAGTGG 5273

## RESULT 4

US-09-984-827-93  
; Sequence 93, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 93  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-93

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACAAAGAAACAAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAACAAATTCGG 60  
Db 4773 CACAAAGAAACAAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAACAAATTCGG 4832  
QY 61 ATTATCTGGTGAAGAGTATGTGCAGATCATACCCAAAAGCTTAAAGACAAAGATCTGGG 120  
Db 4833 ATTATCTGGTGAAGAGTATGTGCAGATCATACCCAAAAGCTTAAAGACAAAGATCTGGG 4892  
QY 121 TGAATGAGTTAGGTATGGCGCTTTCCCTGGGTGCAGTAACTCAAGCACTTCCTC 180  
Db 4893 TGAATGAGTTAGGTATGGCGCTTTCCCTGGGTGCAGTAACTCAAGCACTTCCTC 4952  
QY 181 CGAGTCAAGAGTAAATGATGCCATCAACAATGAAGAAACACCTTAAAGCTGGCCAAGG 240  
Db 4953 CGAGTCAAGAGTAAATGATGCCATCAACAATGAAGAAACACCTTAAAGCTGGCCAAGG 5012

Db 4953 CGAGTCAAGAGTAAATGATGCCACCAACAAATGAAGAAACACCTTAAGCTGCCAAGG 5012  
QY 241 ACAGTTCTCGACATCGATTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
Db 5013 ACAGTTCTCGACATCGATTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
QY 301 GAAATAATCTCAAGGTGTGGTTCAATAACAAGGGTGGCATGCAATCAGCTCTTCCCTGA 360  
Db 5073 GAAATAATCTCAAGGTGTGGTTCAATAACAAGGGTGGCATGCAATCAGCTCTTCCCTGA 5132  
QY 361 ATGTCAATCAACATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 420  
Db 5133 ATGTCAATCAACATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCATT 5192  
QY 421 ATGGAATTAATCTGTTTCAATCATFCCCTGAAATCTCACCAGGAGGCTCTCAGAGGTGG 480  
Db 5193 ATGGAATTAATCTGTTTCAATCATFCCCTGAAATCTCACCAGGAGGCTCTCAGAGGTGG 5252  
QY 481 CTCTGATGACCACATCAGTGG 501  
Db 5253 CTCCGATGACCACATCAGTGG 5273

## RESULT 5

US-09-984-827-94  
; Sequence 94, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 94  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-94

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACAAAGAAACAAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAACAAATTCGG 60  
Db 4773 CACAAAGAAACAAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAACAAATTCGG 4832  
QY 61 ATTATCTGGTGAAGAGTATGTGCAGATCATACCCAAAAGCTTAAAGACAAAGATCTGGG 120  
Db 4833 ATTATCTGGTGAAGAGTATGTGCAGATCATACCCAAAAGCTTAAAGACAAAGATCTGGG 4892  
QY 121 TGAATGAGTTAGGTATGGCGCTTTCCCTGGGTGCAGTAACTCAAGCACTTCCTC 180  
Db 4893 TGAATGAGTTAGGTATGGCGCTTTCCCTGGGTGCAGTAACTCAAGCACTTCCTC 4952  
QY 181 CGAGTCAAGAGTAAATGATGCCATCAACAATGAAGAAACACCTTAAAGCTGGCCAAGG 240  
Db 4953 CGAGTCAAGAGTAAATGATGCCATCAACAATGAAGAAACACCTTAAAGCTGGCCAAGG 5012



Db 5013 ACAGTTCTGCAGATCGATTTCACACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
QY 301 GAAATAATGTCAGAGTGTGGTTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCTCTGA 360  
Db 5073 GAAATAATGTCAGAGTGTGGTTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCTCTGA 5132  
QY 361 ATGTCATCAACAATGCCATTCTCGGGGCCAACCTGCAAAAGGGAGAGAACCTTAGCCATT 420  
Db 5133 ATGTCATCAACAATGCCATTCTCGGGGCCAACCTGCAAAAGGGAGAGAACCTTAGCCATT 5192  
QY 421 ATGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGGAGAGCTCTCAGAGGTGG 480  
Db 5193 ATGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGGAGAGCTCTCAGAGGTGG 5252  
QY 481 CTCTGATGACCACATCAGTGG 501  
Db 5253 CTCCGATGACCACATCAGTGG 5273

## RESULT 8

US-09-984-827-97

; Sequence 97, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFELE, PATRICE

; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984,827

; PRIOR FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108

; PRIOR FILING DATE: 2000-12-11

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 97

; LENGTH: 9870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7138)

; OTHER INFORMATION: a, t, c or g

US-09-984-827-97

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACAAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGGAGCAAGAAACATTTCCG 60  
Db 4773 CACAAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGGAGCAAGAAACATTTCCG 4832  
QY 61 ATTATCTGTTGAAGACGTATGTCAGATCATGCCAAAAGCTTAAAGAAACAAGATCTGGG 120  
Db 4833 ATTATCTGTTGAAGACGTATGTCAGATCATGCCAAAAGCTTAAAGAAACAAGATCTGGG 4892  
QY 121 TGAATGAGTTAGTATGGGGCTTTTCCTGGGTGCAGTAACTCAAGCACTTCCTC 180  
Db 4893 TGAATGAGTTAGTATGGGGCTTTTCCTGGGTGCAGTAACTCAAGCACTTCCTC 4952  
QY 181 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTTAAAGCTGGCCAAAG 240  
Db 4953 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTTAAAGCTGGCCAAAG 5012  
QY 241 ACAGTTCTGCAGATCGATTTCACACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300

Db 5013 ACAGTTCTGCAGATCGATTTCACACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
QY 301 GAAATAATGTCAGAGTGTGGTTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCTCTGA 360  
Db 5073 GAAATAATGTCAGAGTGTGGTTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCTCTGA 5132  
QY 361 ATGTCATCAACAATGCCATTCTCGGGGCCAACCTGCAAAAGGGAGAGAACCTTAGCCATT 420  
Db 5133 ATGTCATCAACAATGCCATTCTCGGGGCCAACCTGCAAAAGGGAGAGAACCTTAGCCATT 5192  
QY 421 ATGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGGAGAGCTCTCAGAGGTGG 480  
Db 5193 ATGGAATTACTGTTTCAATCATCCCTGAATCTCACCAGGAGAGCTCTCAGAGGTGG 5252  
QY 481 CTCTGATGACCACATCAGTGG 501  
Db 5253 CTCCGATGACCACATCAGTGG 5273

## RESULT 9

US-09-984-827-98

; Sequence 98, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFELE, PATRICE

; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984,827

; PRIOR FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108

; PRIOR FILING DATE: 2000-12-11

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 98

; LENGTH: 9870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7138)

; OTHER INFORMATION: a, t, c or g

US-09-984-827-98

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACAAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGGAGCAAGAAACATTTCCG 60  
Db 4773 CACAAAGAAACAAACACTGCAGATATCCTTCAGACCTGCAGGAGCAAGAAACATTTCCG 4832  
QY 61 ATTATCTGTTGAAGACGTATGTCAGATCATGCCAAAAGCTTAAAGAAACAAGATCTGGG 120  
Db 4833 ATTATCTGTTGAAGACGTATGTCAGATCATGCCAAAAGCTTAAAGAAACAAGATCTGGG 4892  
QY 121 TGAATGAGTTAGTATGGGGCTTTTCCTGGGTGCAGTAACTCAAGCACTTCCTC 180  
Db 4893 TGAATGAGTTAGTATGGGGCTTTTCCTGGGTGCAGTAACTCAAGCACTTCCTC 4952  
QY 181 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTTAAAGCTGGCCAAAG 240  
Db 4953 CGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAACACCTTAAAGCTGGCCAAAG 5012  
QY 241 ACAGTTCTGCAGATCGATTTCACACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
Db 5013 ACAGTTCTGCAGATCGATTTCACACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072

QY 301 GAAATAATGTCAGAGTGGTTCATTAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360  
 |||||  
 Db 5073 GAAATAATGTCAGAGTGGTTCATTAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132  
 |||||  
 QY 361 ATGTCATCAACAATGCCATCTCCGGGCCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 420  
 |||||  
 Db 5133 ATGTCATCAACAATGCCATCTCCGGGCCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 5192  
 |||||  
 QY 421 ATGGAATTACTGCTTTCATATCACCCTGAAATCTCACCAGCAGAGCTCTCAGAGGTGG 480  
 |||||  
 Db 5193 ATGGAATTACTGCTTTCATATCACCCTGAAATCTCACCAGCAGAGCTCTCAGAGGTGG 5252  
 |||||  
 QY 481 CTCTGATGACCAATCAGTGG 501  
 |||||  
 Db 5253 CTCGGATGACCAATCAGTGG 5273  
 |||||

RESULT 10  
 US-09-984-827-99  
 ; Sequence 99, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFELE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984.827  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 99  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-99

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
 Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CACAAGAAAAAACAACACTGCAGATATCCTTCAGGACCTGACAGGAGAGAAACATTTTCGG 60  
 |||||  
 Db 4773 CACAAGAAAAAACAACACTGCAGATATCCTTCAGGACCTGACAGGAGAGAAACATTTTCGG 4832  
 |||||  
 QY 61 ATTATCTGGTGAAGACGATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 120  
 |||||  
 Db 4833 ATTATCTGGTGAAGACGATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 4892  
 |||||  
 QY 121 TGAATGAGTTTAGTATGGCGGCTTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 180  
 |||||  
 Db 4893 TGAATGAGTTTAGTATGGCGGCTTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 4952  
 |||||  
 QY 181 CGAGTCAGAGAGTTAATGATGCCATCAACAAGTAAGAACACCTTAAAGCTGGCCAAAG 240  
 |||||  
 Db 4953 CGAGTCAGAGAGTTAATGATGCCATCAACAAGTAAGAACACCTTAAAGCTGGCCAAAG 5012  
 |||||  
 QY 241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTTATGACAGGACTGGACACCA 300  
 |||||  
 Db 5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTTATGACAGGACTGGACACCA 5072  
 |||||

QY 301 GAAATAATGTCAGAGTGGTTCATTAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360  
 |||||  
 Db 5073 GAAATAATGTCAGAGTGGTTCATTAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 5132  
 |||||  
 QY 361 ATGTCATCAACAATGCCATCTCCGGGCCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 420  
 |||||  
 Db 5133 ATGTCATCAACAATGCCATCTCCGGGCCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 5192  
 |||||  
 QY 421 ATGGAATTACTGCTTTCATATCACCCTGAAATCTCACCAGCAGAGCTCTCAGAGGTGG 480  
 |||||  
 Db 5193 ATGGAATTACTGCTTTCATATCACCCTGAAATCTCACCAGCAGAGCTCTCAGAGGTGG 5252  
 |||||  
 QY 481 CTCTGATGACCAATCAGTGG 501  
 |||||  
 Db 5253 CTCGGATGACCAATCAGTGG 5273  
 |||||

RESULT 11  
 US-09-984-827-100  
 ; Sequence 100, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFELE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984.827  
 ; CURRENT FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 100  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-100

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
 Best Local Similarity 99.8%; Pred. No. 4.9e-153;  
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CACAAGAAAAAACAACACTGCAGATATCCTTCAGGACCTGACAGGAGAGAAACATTTTCGG 60  
 |||||  
 Db 4773 CACAAGAAAAAACAACACTGCAGATATCCTTCAGGACCTGACAGGAGAGAAACATTTTCGG 4832  
 |||||  
 QY 61 ATTATCTGGTGAAGACGATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 120  
 |||||  
 Db 4833 ATTATCTGGTGAAGACGATGTGCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 4892  
 |||||  
 QY 121 TGAATGAGTTTAGTATGGCGGCTTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 180  
 |||||  
 Db 4893 TGAATGAGTTTAGTATGGCGGCTTTTCCCTGGGTGTCAGTAATCTCAAGCACTTCCTC 4952  
 |||||  
 QY 181 CGAGTCAGAGAGTTAATGATGCCATCAACAAGTAAGAACACCTTAAAGCTGGCCAAAG 240  
 |||||  
 Db 4953 CGAGTCAGAGAGTTAATGATGCCATCAACAAGTAAGAACACCTTAAAGCTGGCCAAAG 5012  
 |||||  
 QY 241 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTTATGACAGGACTGGACACCA 300  
 |||||  
 Db 5013 ACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTTATGACAGGACTGGACACCA 5072  
 |||||  
 QY 301 GAAATAATGTCAGAGTGGTTCATTAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGA 360  
 |||||



Db 5073 GAAATAATGTCAGGTGTGGTTCAATAACAAAGGCTGGCATGCAATCAGCTCTTTCTGGA 5132  
QY 361 ATGTCTATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCTAGCCATT 420  
Db 5133 ATGTCTATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCTAGCCATT 5192  
QY 421 ATGGAATTAATCTGTTTCAATCATCCCTGAAATCTCACCAGGAGAGCTCTCAGAGTGG 480  
Db 5193 ATGGAATTAATCTGTTTCAATCATCCCTGAAATCTCACCAGGAGAGCTCTCAGAGTGG 5252  
QY 481 CTCTGATGACCAATCAGTGG 501  
Db 5253 CTCCGATGACCAATCAGTGG 5273

RESULT 12  
US-09-984-827-101  
; Sequence 101, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 101  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-101

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 60  
Db 4773 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 4832  
QY 61 ATTATCTGGTGAAGAGTATGTCAGATCATAGCCAAAAGCTTAAAGAACAGATCTGGG 120  
Db 4833 ATTATCTGGTGAAGAGTATGTCAGATCATAGCCAAAAGCTTAAAGAACAGATCTGGG 4892  
QY 121 TGAATCAGTTAGGTATGGGCTTTTCCCTGGTCTAGTAACTCAAGCACTTCCTC 180  
Db 4893 TGAATCAGTTAGGTATGGGCTTTTCCCTGGTCTAGTAACTCAAGCACTTCCTC 4952  
QY 181 CGAGTCAAGAAGTTAATGATGCCATCAAAACAAATGAAGAACACCTTAAAGCTGGCCAAAG 240  
Db 4953 CGAGTCAAGAAGTTAATGATGCCATCAAAACAAATGAAGAACACCTTAAAGCTGGCCAAAG 5012  
QY 241 ACAGTCTGCAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
Db 5013 ACAGTCTGCAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
QY 301 GAAATAATGTCAGGTGTGGTTCAATAACAAAGGCTGGCATGCAATCAGCTCTTTCTGGA 360

Db 5073 GAAATAATGTCAGGTGTGGTTCAATAACAAAGGCTGGCATGCAATCAGCTCTTTCTGGA 5132  
QY 361 ATGTCTATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCTAGCCATT 420  
Db 5133 ATGTCTATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCTAGCCATT 5192  
QY 421 ATGGAATTAATCTGTTTCAATCATCCCTGAAATCTCACCAGGAGAGCTCTCAGAGTGG 480  
Db 5193 ATGGAATTAATCTGTTTCAATCATCCCTGAAATCTCACCAGGAGAGCTCTCAGAGTGG 5252  
QY 481 CTCTGATGACCAATCAGTGG 501  
Db 5253 CTCCGATGACCAATCAGTGG 5273

RESULT 13  
US-09-984-827-102  
; Sequence 102, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 102  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-102

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 60  
Db 4773 CACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 4832  
QY 61 ATTATCTGGTGAAGAGTATGTCAGATCATAGCCAAAAGCTTAAAGAACAGATCTGGG 120  
Db 4833 ATTATCTGGTGAAGAGTATGTCAGATCATAGCCAAAAGCTTAAAGAACAGATCTGGG 4892  
QY 121 TGAATCAGTTAGGTATGGGCTTTTCCCTGGTCTAGTAACTCAAGCACTTCCTC 180  
Db 4893 TGAATCAGTTAGGTATGGGCTTTTCCCTGGTCTAGTAACTCAAGCACTTCCTC 4952  
QY 181 CGAGTCAAGAAGTTAATGATGCCATCAAAACAAATGAAGAACACCTTAAAGCTGGCCAAAG 240  
Db 4953 CGAGTCAAGAAGTTAATGATGCCATCAAAACAAATGAAGAACACCTTAAAGCTGGCCAAAG 5012  
QY 241 ACAGTCTGCAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
Db 5013 ACAGTCTGCAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
QY 301 GAAATAATGTCAGGTGTGGTTCAATAACAAAGGCTGGCATGCAATCAGCTCTTTCTGGA 360  
Db 5073 GAAATAATGTCAGGTGTGGTTCAATAACAAAGGCTGGCATGCAATCAGCTCTTTCTGGA 5132

QY 361 ATGTCATCAACAATGCCATTCTCCGGGCGCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 420  
 |||||  
 Db 5133 ATGTCATCAACAATGCCATTCTCCGGGCGCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 5192  
 |||||  
 QY 421 ATGGAATTACTGCTTTCAATCATATCCCTGAAATCTCACCAGGAGCAGCTCTCAGAGGTGG 480  
 |||||  
 Db 5193 ATGGAATTACTGCTTTCAATCATATCCCTGAAATCTCACCAGGAGCAGCTCTCAGAGGTGG 5252  
 |||||  
 QY 481 CTCTGATGACCATCATCAGTGG 501  
 |||||  
 Db 5253 CTCCGATGACCATCATCAGTGG 5273  
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## RESULT 14

US-09-984-827-103  
 ; Sequence 103, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFELE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984,827  
 ; PRIOR FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 103  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-103

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
 Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 Db 4833 ATTATCTGGTGAAGACGCTATGTCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 4892  
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 QY 121 TGAATGAGTTTATGATGGCGCTTTTCCCTGGGTGCAGTAATCTCAAGCACTTCCCTC 180  
 |||||  
 Db 4893 TGAATGAGTTTATGATGGCGCTTTTCCCTGGGTGCAGTAATCTCAAGCACTTCCCTC 4952  
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 QY 241 ACAGTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 300  
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 Db 5013 ACAGTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCA 5072  
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 Db 5073 GAAATTAATGTCAGAGTGTGGTTCAATTAACAAGGGCTGGCATGCAATCAGCTCTTTCTCTGA 5132  
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QY 361 ATGTCATCAACAATGCCATTCTCCGGGCGCAACCTGCAAAAGGAGAGAACCCCTAGCCATT 420  
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 Db 5253 CTCCGATGACCATCATCAGTGG 5273  
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## RESULT 15

US-09-984-827-104  
 ; Sequence 104, Application US/09984827  
 ; Publication No. US20030056234A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DENEFELE, PATRICE  
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
 ; APPLICANT: DUVERGER, NICOLAS  
 ; APPLICANT: CAMBIEN, FRANCOIS  
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
 ; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
 ; FILE REFERENCE: 03806.0522-00000  
 ; CURRENT APPLICATION NUMBER: US/09/984,827  
 ; PRIOR FILING DATE: 2002-04-01  
 ; PRIOR APPLICATION NUMBER: 60/254,108  
 ; PRIOR FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: FR 00/14037  
 ; PRIOR FILING DATE: 2000-10-31  
 ; NUMBER OF SEQ ID NOS: 161  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 104  
 ; LENGTH: 9870  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: (7138)  
 ; OTHER INFORMATION: a, t, c or g  
 US-09-984-827-104

Query Match 99.4%; Score 497.8; DB 9; Length 9870;  
 Best Local Similarity 99.6%; Pred. No. 4.9e-153;  
 Matches 499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CACAAGAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 60  
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 Db 4773 CACAAGAAACAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTTCGG 4832  
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 |||||  
 Db 4833 ATTATCTGGTGAAGACGCTATGTCAGATCATAGCCAAAGCTTAAAGAACAGATCTGGG 4892  
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 Db 4893 TGAATGAGTTTATGATGGCGCTTTTCCCTGGGTGCAGTAATCTCAAGCACTTCCCTC 4952  
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Job time : 79.6923 secs

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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 566.323 Seconds  
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estcov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_nus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2          | 308.8 | 61.6        | 381    | 12    | BE757461    |
| 3          | 173   | 34.5        | 376    | 12    | BF855659    |
| 4          | 161.4 | 32.2        | 1089   | 12    | BE905243    |
| 5          | 142.8 | 28.5        | 1132   | 12    | BE786243    |
| 6          | 127.6 | 25.5        | 882    | 14    | BQ948089    |

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| 8  | 111   | 22.2 | 423  | 14 | BM687039 |
| 9  | 110   | 22.0 | 452  | 14 | W26316   |
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| 11 | 98.4  | 19.6 | 281  | 13 | BI063291 |
| 12 | 90.2  | 18.0 | 434  | 10 | AW322690 |
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DEFINITION MR3-HT0737-060700-004-b09 HT0737 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE715104  
VERSION BE715104.1 GI:10103369  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

#### REFERENCE

#### AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 463)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Anconio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001



LOCUS BF855659 376 bp mRNA linear EST 16-JAN-2001  
DEFINITION RC6-FN0202-171100-012-D01 FN0202 Homo sapiens cDNA, mRNA sequence.  
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VERSION BF855659.1 GI:12243403  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 376)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml.pl?cl=RC6t2-RC6-FN0202-  
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Research) profiles into the puc 18 vector. Reverse  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1089)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9701 row: h column: 22  
High quality sequence stop: 652.  
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Technologies."  
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Best Local Similarity 57.7%; Pred. No. 5.5e-34;  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1132)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DPF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9639 row: k column: 20
High quality sequence stop: 695.
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/lab_host="DH10B (phage-resistant)"
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Technologies."
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| | | | | | | | | | | | | | | |

QY 304 ATATGTCAAGGTGTGTTCAATACAGAGGCTGCGATGCAATCAGCTCTTTCTGTAATG 363
| | | | | | | | | | | | | | | |

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Db 307 ACAACATTAAGTGTGTGTTTAATAACAAAGCTGGCATGCCCTGTGTCAGCTTTCTCAATG 366
| | | | | | | | | | | | | | | |
QY 364 TCATCAACAATGCCATTCCTCGGGCCAAACCTGCAAAAGGAGAGAACCCCTAGCCATTATG 423
| | | | | | | | | | | | | | | |
Db 367 TGGCCACACAGCCATCTTACGGCCAGCCCTGCTAGGACAGAGCCCGGAGGATG 426
| | | | | | | | | | | | | | | |

QY 424 GAATTAATGCTTTCAATCATCCCTGAATCTACACAGCAGCAGCTCTCAGAGTGGCTC 483
| | | | | | | | | | | | | | | |
Db 427 GAATCAGCTGATAGCAACCCCTGAACCTGACCAAGGAGCAGCTCTCAGAGATTACAG 486
| | | | | | | | | | | | | | | |

QY 484 TGATGACCACATCAGTGG 501
| | | | | | | | | | | | | | | |
Db 487 TGCTGACCACCTTCAGTGG 504
| | | | | | | | | | | | | | | |

RESULT 6
BQ948089 882 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT_8800681 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6392328
DEFINITION 5', mRNA sequence.
ACCESSION BQ948089
VERSION BQ948089.1 GI:22363567
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1382 row: a column: 01
High quality sequence stop: 768.
FEATURES
Location/Qualifiers
1..882
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6392328"
/clone_lib="NIH_MGC_130"
/lab_host="DH10B (phage-resistant)"
/note="Organ: otcysts; Vector: pCMV-SPORT6.1.cdb;
Site:1: EcoRV; Site:2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
NIH_MGC Library."
BASE COUNT 176 a 269 c 251 g 185 t
ORIGIN
Query Match 25.5%; Score 127.6; DB 14; Length 882;
Best Local Similarity 55.6%; Pred. No. 1.2e-24;
Matches 266; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

QY 24 GATATCTTCAGACCTGACAGGAGAAACATTCGATTTATCTGGTGAAGACGTATG 83
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Db 332 GAGGTGTCCAGAACCTCACTGCGCCGAAATGTGTCTCACTTTTGTGTAAGACATACCC 391
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QY 84 CAGATCATAGCCAAAAGCTTAAAGAACAGATCTGGTGAATCAGTTAGGTATGCGGC 143
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Db 392 AGCTGTGTCGCGAGCCCTTAAGACCAAGAGTGGTGGATGAGTCAAGTATGGGGC 451
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QY 144 TTTTCCCTGGGTCTAGTAACTCAAGCACTTCCTCCGAGTCAAGAGTTAATGATGCC 203
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Db 452 TTCTCCTGGGAGCGCGAGA---TCCAGACCTGCCACAGGCGCATGAGGTGGTCCGCACA 508
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QY 204 ATCAACAATAAGAAACACACCTAAAGCTGGCCAAAGGACAGTCTGCAGATGCAATGCTTC 263
Db 509 TTGGCAGAGATTGCGGCACCTGCTGAGCCGCCACCTGGGAATGCCCTAGACCGTATCTCG 568
QY 264 ACACGCTTGGGAAGATTATACAGAGACTGGACACAGCAAAATAATGTCAGAGTGTGGTTC 323
Db 569 ACAACCTCACTACGTCAGTGGGCCCTTGCCCTTGATGTCGGAACAGAGCTCAAGATCTGGTC 628
QY 324 AATAACAAGGCTGGCATGCAATCACTAGCTCTTTCTCTGGAATGTCATCAACAATGCCATTC 383
Db 629 ACACACAGGCTGGCATGCCATGCTGGCTTTGTGACCCGAGCCAAATGAGGACTCTTA 688
QY 384 CGGGCCACCTCAAAAGGAGAGAACCTAGCCATTAATGGAATTAATGCTTTCAATCAT 443
Db 689 CATGCCCTCTACCATCTGCTGCTCCAGCTCCGCCATGCCACAGCATCACTACATCAACCAT 748
QY 444 CCCCTGAATCTCACAAGCAGCAGCTCTCAGAGGTGGCTCTGATGACACCATCACTGG 501
Db 749 CTTTGAAGCTGACCAAGGAGAGCTATCTGAAGCTACACTGATAGCTCCGCCCTCTGG 806

RESULT 7
LOCUS U66691 2640 bp mRNA linear HTC 23-JUL-2001
DEFINITION Homo sapiens clone EST394388 mRNA sequence.
ACCESSION U66691
VERSION U66691.1 GI:1906576
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2640)
AUTHORS Allikmets R., Gerrard B., Hutchinson A. and Dean M.
TITLE Characterization of the human ABC superfamily: isolation and
mapping of 21 new genes using the expressed sequence tags database
JOURNAL Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
MEDLINE 97049974
PUBMED 8894702
REFERENCE 2 (bases 1 to 2640)
AUTHORS Allikmets R., Gerrard B. and Dean M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer
Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES
Location/Qualifiers
Source 1..2640
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="EST394388"
/note="similar to ATP-binding cassette transporter"

BASE COUNT 607 a 672 c 567 g 647 t 47 others
ORIGIN

Query Match 23.7%; Score 118.8; DB 11; Length 2640;
Best Local Similarity 55.8%; Pred. No. 4.3e-22;
Matches 242; Conservative 0; Mismatches 191; Indels 1; Gaps 1;

QY 69 GTGAAGACGTATGTCAGATCATATGCCAAAGCTTAAAGAACAGATCTGGTGAATGATG 128
Db 988 GNGAGTANNATCTGCTTATAGACAGCCTTAAGACGAATTTGGTCAATGAA 1047
QY 129 TTTAGTATGCGGGCTTTTCCTGGGTGTCAGTAATACTCAAGCACTTCTCCCGAGTCAA 188
Db 1048 CAGAGGTATGGAGGAATTTCCATTTGGAGGAAGCTCCAGTCTGCCCATCAGGGGGAA 1107
QY 189 GAAGTATATGATGCCATCAACAATGAAGAACACCTTAAGCTGGCCAGGACAGATCTCT 248
Db 1108 GCACITGTGGGTGTTTAAAGCAGCTTGGCGGATCATGAATGTGAGCGGGGCCCTATC 1167
QY 249 CGAGATCGATTTCTCAACAGCTTGGGAGATTTATGACAGGACTGGACACCAAGAAATAT 308
Db 1168 ACTAGAGAGGCTCTTAAGAAATACCTGATTTCCCTTACATCTAGAACTAGACACAC 1227
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QY 309 GTCAGGTGTGTTCAATAACAAGGCTGGCATCAATCAGCTCTTCTCCTGAATGCTATC 368
Db 1228 ATTAAGTGTGTTTATAACAAGGCTGGCATGCCCTGGTCACTTTCTCAATGTGGCC 1287
QY 369 AACAAATGCCATTCCGGGCCAACCTCAAAAGGAGAGAACCCCTAGCCATTAATGGAATT 428
Db 1288 CACAACGCCATCTTACGGGCCAGGCTGCTTAAGGACAGAGCCGCCGAGGATATGGAATC 1347
QY 429 ACTGCTTTCAATCATCCCTCAATCT-CACCAAGCAGCAGCTCTCAGAGTGGCTCTGAT 487
Db 1348 ACGTCAATGACCAACCCCTGAACCTGGACCAAGGAGCAGCTCTCAGAGATTACAGTCT 1407
QY 488 GACCACATCACTGG 501
Db 1408 GACCACTTCAGTGG 1421

RESULT 8
LOCUS BM687039 423 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CQ1-acx-g-10-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-acx-g-10-0-UI 5', mRNA sequence.
ACCESSION BM687039
VERSION BM687039.1 GI:19000297
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Bonaldo M.F., Lennon G. and Soares M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
Source 1..423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-acx-g-10-0-UI"
/clone_lib="UI-E-CQ1"
/tissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site: 1: EcoR I; Site 2: Not I;
UI-E-CQ1 is a normalized cDNA library containing the
following tissue(s): optic nerve. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA,
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CCATTAAGTG. This library was created for the program, Gene
```



|            |           |           |         |
|------------|-----------|-----------|---------|
| RESULT 12  | ACCESSION | REFERENCE | JOURNAL |
| AW322690   | VERSION   | AUTHORS   | COMMENT |
| LOCUS      | KEYWORDS  | TITLE     |         |
| DEFINITION | SOURCE    |           |         |
|            | ORGANISM  |           |         |

FEATURES SOURCE

BASE COUNT  
ORIGIN

|            |           |
|------------|-----------|
| RESULT 13  | ACCESSION |
| CNS03550/  | VERSION   |
| LOCUS      | KEYWORDS  |
| DEFINITION | SOURCE    |
|            | ORGANISM  |

|                           |   |
|---------------------------|---|
| JOURNAL                   | Unpublished   |
| REFERENCE                 | 2 (bases 1 to 875)  |
| AUTHORS                   | Roest-Crolius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.   |
| TITLE                     | Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  |
| JOURNAL                   | Unpublished   |
| REFERENCE                 | 3 (bases 1 to 875)  |
| AUTHORS                   | Genoscope.  |
| TITLE                     | Direct Submission   |
| JOURNAL                   | Submitted (12-APR-2000)   |
| COMMENT                   | This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.   |
| FEATURES                  | Location/Qualifiers   |
| source                    | 1..875  |
|                           | /organism="Tetraodon nigroviridis"  |
|                           | /db_xref="taxon:99883"  |
|                           | /clone="132012"   |
|                           | /clone_lib="c"  |
|                           | /note="Genoscope sequence ID : COAG132BH06SP1-end ; PUC-Ori"  |
| BASE COUNT                | 179 a 243 c 238 g 206 t 9 others  |
| ORIGIN                    |   |
| Query Match               | 17.5% ; Score 87.8; DB 17; Length 875;  |
| Best Local Similarity     | 68.8%; Pred. No. 1.3e-13;   |
| Matches 119; Conservative | 1; Mismatches 53; Indels 0; Gaps 0;   |
| Qy 313                    | AGGTGTTGGTCAATAACAAAGGCTGGCATCGAATCAGCTCTTTTCCTGAATGTCATCAACA 372<br>   |
| Db 475                    | AGGTGTTGGTACATAACAAASGGCTGGCACGCCATGGTGCTTCATCAACGTGCCTAACCA 534<br>  |
| Qy 373                    | ATGCCATTCTCCGGGGCAACTGTGAAAAGGAGAGAACCTTAGCCATTATGGAAATTACTG 432<br>  |
| Db 535                    | ACGCATCTCTGGCGGGAACCTGCCCGACGGCCAACCTGGCGGAACACGGCATCACGG 594<br>   |
| Qy 433                    | CTTTCAATCATCCCTCAATCTCACCAGGACGACCTCTCAGAGTGCGTCTG 485<br>  |
| Db 595                    | TGATCACCATCTCTGAACTGACCAAGNGACAGCTGTCCGAGATCACTGTG 647<br>  |
| RESULT 15                 |   |
| H87069                    |   |
| LOCUS                     | H87069 426 bp mRNA linear EST 21-NOV-1995   |
| DEFINITION                | IMAGE4805.r1 Soares retina N2B4HR Homo sapiens CDNA clone   |
| ACCESSION                 | H87069  |
| VERSION                   | H87069.1 GI:1068648   |
| KEYWORDS                  | EST.  |
| SOURCE                    | human.  |
| ORGANISM                  | Homo sapiens  |
|                           | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.<br>1 (bases 1 to 426)<br>Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman<br>M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J.,<br>Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston<br>R., Williamson,A., Wohlmann,P. and Wilson,R.<br>The WashU-Merck EST Project<br>Unpublished (1995)<br>Contact: Wilson RK<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@watson.wustl.edu<br>High quality sequence stops: 330<br>Source: IMAGE Consortium, LLNL<br>This clone is available royalty-free through LLNL ; contact the<br>IMAGE Consortium (info@image.llnl.gov) for further information. |

Insert Length: 1209 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 330.  
Location/Qualifiers  
1. 426  
/organism="Homo sapiens"  
/db\_xref="GDB:3848514"  
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/clone="IMAGE:220521"  
/clone\_lib="Soares retina N2b4HR"  
/sex="male"  
/tissue.type="retina"  
/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: eye; Vector: pFR73D (Pharmacia) with a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pFR73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES  
Source

|                           |   |       |       |       |          |
|---------------------------|---|-------|-------|-------|----------|
| BASE COUNT                | 117 a   | 100 c | 105 g | 101 t | 3 others |
| ORIGIN                    |   |       |       |       |          |
| Query Match               | 16.7%; Score 83.8; DB 14; Length 426;                             |       |       |       |          |
| Best Local Similarity     | 54.1%; Pred. No. 1.4e-12;   |       |       |       |          |
| Matches 213; Conservative | 0; Mismatches 178; Indels 3; Gaps 2;                              |       |       |       |          |
| QY 88                     | TATATGCCAAAGCTTAAAGACACAGATCTGGTGAATGAGTTAGGTATGGCGGCTTTT 147     |       |       |       |          |
| DB 11                     | TTTTATAAGAGCAGCTTAAAGACAAATCTGGGTCAATGACAGAGGTATGGAGGAATTT 70     |       |       |       |          |
| QY 148                    | CCCTGGGTGTCAGTATATCTCAAGACACTTCCCGGCTCAAGAAGTTAATGATGCCATCA 207   |       |       |       |          |
| DB 71                     | CCATTGGAGGAAGCTCCAGTCGTCCCATCACGGGGGAGACACTTGTGGGTTTTTAA 130      |       |       |       |          |
| QY 208                    | AACAAATGAAGAACACCTTAAAGCTGGCCAGGACAGTTCCTGCAGATCCGATTTCTCAACA 267 |       |       |       |          |
| DB 131                    | GCGACCTTGGCCGGATCATGAATGTGAGCGGGGGCCCTATCATCTAGAGAGGCTCTAAAG 190  |       |       |       |          |
| QY 268                    | GCTTGGGAAGATTTATGACGAGCTGGACACCAAGAAATATGTCAAGGTGTGTTCAATA 327    |       |       |       |          |
| DB 191                    | AAATACCTGATTTCTTAAACATCTAGAAGCTGACACAAATTAAGGTGGTTTAATA 250       |       |       |       |          |
| QY 328                    | ACAAGGCTGGCATGCAATCAGCTTTCTGAACTCATCAACAATGCCATTCTCCGGG 387       |       |       |       |          |
| DB 251                    | ACAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAATGTGGCCACACGCCCATCTTACGGG 310   |       |       |       |          |
| QY 388                    | CCAAACC-TGCARAGGAGACCCCTAGCCATTATGGAATTAC--TGCTTTCAATCATC 444     |       |       |       |          |
| DB 311                    | CCAGCCTTGCTTAAGGACAGGAGCCCGGAGGATGTGGAATCACCCTTCATTAGCAACC 370    |       |       |       |          |
| QY 445                    | CCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGT 478                            |       |       |       |          |
| DB 371                    | CCTGNACCTGGACCAAGGAGCAGCTCTCAGAGAT 404                            |       |       |       |          |

Search completed: April 3, 2003, 16:36:54  
Job time : 573.323 secs

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GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 992.885 Seconds  
(without alignments)  
14684.987 Million cell updates/sec

Title: US-09-595-526c-1\_COPY\_7250\_7750

Perfect score: 501

Sequence: 1 ttacaggggcagtgccctttg.....tggtggcagtaacatgcaac 501

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vt.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_ma.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_pat.\*  
23: em\_ov.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vt.\*  
30: em\_hgt\_hum.\*  
31: em\_hgt\_inv.\*  
32: em\_hgt\_other.\*  
33: em\_hgt\_mus.\*  
34: em\_hgt\_pln.\*  
35: em\_hgt\_rod.\*  
36: em\_hgt\_man.\*  
37: em\_hgt\_vrt.\*  
38: em\_sy.\*  
39: em\_hgt\_hum.\*  
40: em\_hgt\_mus.\*  
41: em\_hgtc\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description |
|------------|-------|-------------|--------|----|----------|-------------|
| 1          | 501   | 100.0       | 2617   | 6  | AX059974 | Sequence    |
| 2          | 501   | 100.0       | 2894   | 6  | AX127797 | Sequence    |
| 3          | 501   | 100.0       | 2894   | 6  | AX139784 | Sequence    |
| 4          | 501   | 100.0       | 3366   | 6  | AX060718 | Sequence    |
| 5          | 501   | 100.0       | 3366   | 6  | AX060897 | Sequence    |
| 6          | 501   | 100.0       | 5352   | 6  | AX127778 | Sequence    |
| 7          | 501   | 100.0       | 5352   | 6  | AX139768 | Sequence    |
| 8          | 501   | 100.0       | 9495   | 6  | AX059978 | Sequence    |
| 9          | 501   | 100.0       | 9497   | 6  | AX059973 | Sequence    |
| 10         | 501   | 100.0       | 9497   | 9  | AF165281 | Homo sapi   |
| 11         | 501   | 100.0       | 9593   | 6  | AX059976 | Sequence    |
| 12         | 501   | 100.0       | 9741   | 6  | AX127830 | Sequence    |
| 13         | 501   | 100.0       | 9741   | 6  | AX139817 | Sequence    |
| 14         | 501   | 100.0       | 9741   | 6  | AX351038 | Sequence    |
| 15         | 501   | 100.0       | 9854   | 6  | AX127831 | Sequence    |
| 16         | 501   | 100.0       | 9854   | 6  | AX139818 | Sequence    |
| 17         | 501   | 100.0       | 10442  | 6  | AX060713 | Sequence    |
| 18         | 501   | 100.0       | 10442  | 6  | AX060892 | Sequence    |
| 19         | 501   | 100.0       | 10442  | 9  | AF285167 | Homo sapi   |
| 20         | 501   | 100.0       | 10474  | 6  | AX060719 | Sequence    |
| 21         | 501   | 100.0       | 10474  | 6  | AX060721 | Sequence    |
| 22         | 501   | 100.0       | 10474  | 6  | AX060898 | Sequence    |
| 23         | 501   | 100.0       | 10474  | 6  | AX060900 | Sequence    |
| 24         | 490   | 97.8        | 7860   | 6  | AX092594 | Sequence    |
| 25         | 490   | 97.8        | 7862   | 6  | AX135712 | Sequence    |
| 26         | 490   | 97.8        | 129608 | 9  | AL353685 | Human DNA   |
| 27         | 490   | 97.8        | 149034 | 9  | AF275948 | Homo sapi   |
| 28         | 490   | 97.8        | 182012 | 9  | AL359846 | Human DNA   |
| 29         | 490   | 97.8        | 183999 | 6  | AX092589 | Sequence    |
| 30         | 490   | 97.8        | 201144 | 9  | AF287262 | Homo sapi   |
| 31         | 479.4 | 95.7        | 5097   | 9  | BD012346 | Genes rel   |
| 32         | 479.4 | 95.7        | 5097   | 9  | AK027864 | Homo sapi   |
| 33         | 479.4 | 95.7        | 5097   | 23 | BD005026 | Genes rel   |
| 34         | 479.2 | 95.6        | 2011   | 6  | AX060717 | Sequence    |
| 35         | 479.2 | 95.6        | 2011   | 6  | AX060896 | Sequence    |
| 36         | 225.4 | 45.0        | 151159 | 2  | AC098668 | Sequence    |
| 37         | 197.4 | 39.4        | 7878   | 10 | MMABC1   | Sequence    |
| 38         | 197.4 | 39.4        | 186889 | 2  | AL807243 | Mus muscu   |
| 39         | 197.4 | 39.4        | 206695 | 2  | AC091466 | Mus muscu   |
| 40         | 197.4 | 39.4        | 230272 | 2  | AL772397 | Mus muscu   |
| 41         | 197.4 | 39.4        | 278572 | 10 | AF287263 | Mus muscu   |
| 42         | 178   | 35.5        | 748    | 6  | AX060716 | Sequence    |
| 43         | 178   | 35.5        | 748    | 6  | AX060895 | Sequence    |
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## ALIGNMENTS

RESULT 1  
AX059974  
LOCUS AX059974  
DEFINITION Sequence 92 from Patent WO0079970.  
ACCESSION AX059974  
VERSION AX059974.1 GI:12405632  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 2617)  
Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,  
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.  
and Brewer,H.B.

Pred. No. is the number of results predicted by chance to have a

TITLE Nucleic acid and proteinic acids corresponding to human gene abcl  
JOURNAL Patent: WO 0078970-A 92 28-DEC-2000;  
Aventis Pharma S.A. (FR)

## FEATURES

source  
1. .2517  
Location/Qualifiers

BASE COUNT 840 a 459 c 435 g 883 t  
ORIGIN

Query Match 100.0%; Score 501; DB 6; Length 2617;  
Best Local Similarity 100.0%; Pred. No. 3.4e-115;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGCCTTTGTAGCTATGCTTGTATGGCTCTCAAGTCAAAAGACTTGAA 60  
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QY 121 TTGAACCTACACACTTTTTTTTTTTTGTTCCTGCTATTCTCATTTGGGGTTGCAACAAT 180  
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DB 500 CTGGTGGCAGTAACATGCAAC 520

## RESULT 2

AX127797 LOCUS AX127797 2894 bp DNA linear PAT 15-MAY-2001

DEFINITION Sequence 36 from Patent WO0130848.  
ACCESSION AX127797  
VERSION AX127797.1 GI:1413444

## KEYWORDS

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2894)

Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,

Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,

Remaley, A., Brewer, H.B. and Dean, M.

Nucleic acids of the human abcl gene and their therapeutic and

diagnostic application

Patient: WO 0130848-A 36 03-MAY-2001;

Aventis Pharma S.A. (FR)

Location/Qualifiers

1. .2894

/organism="Homo sapiens"

## FEATURES

source

BASE COUNT 922 a 507 c 505 g 959 t 1 others  
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Query Match 100.0%; Score 501; DB 6; Length 2894;  
Best Local Similarity 100.0%; Pred. No. 3.4e-115;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 375 TTTAGTTTTTACCTATACCTATGTAAGTCTATTATGGAACCCCAATGGACATATGGGT 434  
QY 121 TTGAACCTACACACTTTTTTTTTTTTGTTCCTGCTATTCTCATTTGGGGTTGCAACAAT 180  
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QY 181 AATTTCATCAAGTATATGATGCGGAGGATATTGATCAAAATCAAAAGTAAATGCACATCC 240  
DB 495 AATTTCATCAAGTATATGATGCGGAGGATATTGATCAAAATCAAAAGTAAATGCACATCC 554  
QY 241 TCATTCTAAGCCATGCCATGCCAGGAGACTGTTTCCCGGTGACACATCCATTGGTGTG 300  
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DB 675 GTGTCATGCTCAGTTTTTGTGAAAGTCTGCTGCTCAGAGTCTATCAACATTTGAATATCAG 734  
QY 421 TTGACAGATGGTGCCATGCCAGTCAACATCTGCTTTGATTCCTCTGATAAGCTGTT 480  
DB 735 TTGACAGATGGTGCCATGCCAGTCAACATCTGCTTTGATTCCTCTGATAAGCTGTT 794  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
DB 795 CTGGTGGCAGTAACATGCAAC 815

## RESULT 3

AX139784 LOCUS AX139784 2894 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 36 from Patent EP1096012.  
ACCESSION AX139784  
VERSION AX139784.1 GI:14275366

## KEYWORDS

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2894)

Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,

Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,

Remaley, A., Brewer, H.B. and Dean, M.

Nucleic acids of the human abcl gene and their therapeutic and

diagnostic application

Patient: EP 1096012-A 36 02-MAY-2001;

Aventis Pharma S.A. (FR)

Location/Qualifiers

1. .2894

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 922 a 507 c 505 g 959 t 1 others  
ORIGIN

Query Match 100.0%; Score 501; DB 6; Length 2894;  
Best Local Similarity 100.0%; Pred. No. 3.4e-115;



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Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 TTTAGTTTTTACCTATACCTATGTAAGAACTCTATTATGGAACCAATGGACATATGGGT 120
Db 375 TTTAGTTTTTACCTATACCTATGTAAGAACTCTATTATGGAACCAATGGACATATGGGT 434
QY 121 TTGAACCTACACATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 180
Db 435 TTGAACCTACACATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 494
QY 181 AATTTCATCAAGTAATCATGGCCAGCGATTATTATGATCAAAATCAAAAGGTAATGACATCC 240
Db 495 AATTTCATCAAGTAATCATGGCCAGCGATTATTATGATCAAAATCAAAAGGTAATGACATCC 554
QY 241 TCATTCACTAAGCCATGCCATGCCAGGAGCTGTTTCCCGGTGACACATCCATTGGTG 300
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QY 301 GCAATGAGTGTCCAGAGTTATTAGTGCACAGTTTTCAGAAAGTTTGAAGCACCATTGGT 360
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QY 421 TTGACAGAAATGGTGCATGCGTGGCTAACATCCCTGTTTGTATCCCTCTGATAAGCTGTT 480
Db 735 TTGACAGAAATGGTGCATGCGTGGCTAACATCCCTGTTTGTATCCCTCTGATAAGCTGTT 794
QY 481 CTGGTGGCAGTAACATGCAAC 501
Db 795 CTGGTGGCAGTAACATGCAAC 815

RESULT 4
AX060718 AX060718 3366 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 6 from Patent WO0078972.
ACCESSION AX060718
VERSION AX060718.1 GI:12406107
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3366)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abc1 polypeptides
JOURNAL Patent: WO 0078972-A 6 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
Source
1. 3366
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1119 a 564 c 559 g 1120 t 4 others
ORIGIN
Query Match 100.0%; Score 501; DB 6; Length 3366;
Best Local Similarity 100.0%; Pred. No. 3.3e-115;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 174 TTTAGTTTTTACCTATACCTATGTAAGAACTCTATTATGGAACCAATGGACATATGGGT 293
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Db 294 TTGAACCTACACATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 353
QY 181 AATTTCATCAAGTAATCATGGCCAGCGATTATTATGATCAAAATCAAAAGGTAATGACATCC 240
Db 354 AATTTCATCAAGTAATCATGGCCAGCGATTATTATGATCAAAATCAAAAGGTAATGACATCC 413
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QY 181 AATTTCATCAAGTAATCATGGCCAGCGATTATTATGATCAAAATCAAAAGGTAATGACATCC 240
Db 354 AATTTCATCAAGTAATCATGGCCAGCGATTATTATGATCAAAATCAAAAGGTAATGACATCC 413
QY 241 TCATTCACTAAGCCATGCCATGCCAGGAGCTGTTTCCCGGTGACACATCCATTGGTG 300
Db 414 TCATTCACTAAGCCATGCCATGCCAGGAGCTGTTTCCCGGTGACACATCCATTGGTG 473
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Db 474 GCAATGAGTGTCCAGAGTTATTAGTGCACAGTTTTCAGAAAGTTTGAAGCACCATTGGT 533
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QY 481 CTGGTGGCAGTAACATGCAAC 501
Db 654 CTGGTGGCAGTAACATGCAAC 674

RESULT 5
AX060897 AX060897 3366 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 6 from Patent WO0078971.
ACCESSION AX060897
VERSION AX060897.1 GI:12406274
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3366)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abc1 polypeptides
JOURNAL Patent: WO 0078971-A 6 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
Source
1. 3366
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 1119 a 564 c 559 g 1120 t 4 others
ORIGIN
Query Match 100.0%; Score 501; DB 6; Length 3366;
Best Local Similarity 100.0%; Pred. No. 3.3e-115;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTACAGGCGCAGTGCCTTTGTAGCCTATGTCTGTATGCTCCTCAAGTGAAGACTTGAA 60
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 QY 361 GTGTCATGCTACTTTTGTGAAGTGCTGCTGCTCAGAGTCTATCAACATTGAATATCAG 420  
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 QY 421 TTGACAGATGGTCCATGCGGTGCTAATCCTGCTTTGATTCCTCTGATAAGCTGTT 480  
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 LOCUS AX127778 5352 bp DNA linear PAT 15-MAY-2001  
 DEFINITION Sequence 17 from Patent WO0130848.  
 ACCESSION AX127778  
 VERSION AX127778.1 GI:14134425  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5352)  
 AUTHORS Denefle P., Rosier-Montus M.F., Arnould-Reguigne I., Prades C.,  
 Naudin L., Lemoine C., Duverger N., Jaye M., Searfoss G.H.,  
 Remaley A., Brewer H.B. and Dean M.  
 TITLE Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: WO 0130848-A 17 03-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
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 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 3e-115;  
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 LOCUS AX139765 5352 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 17 from Patent EP1096012.  
 ACCESSION AX139765  
 VERSION AX139765.1 GI:14275347  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5352)  
 AUTHORS Denefle P., Rosier-Montus M.F., Arnould-Reguigne I., Prades C.,  
 Naudin L., Lemoine C., Duverger N., Jaye M., Searfoss G.H.,  
 Remaley A., Brewer H.B. and Dean M.  
 TITLE Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: EP 1096012-A 17 02-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
 Location/Qualifiers  
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 Best Local Similarity 100.0%; Pred. No. 3e-115;  
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 RESULT 7  
 LOCUS AX139765 5352 bp DNA linear PAT 30-MAY-2001  
 DEFINITION Sequence 17 from Patent EP1096012.  
 ACCESSION AX139765  
 VERSION AX139765.1 GI:14275347  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5352)  
 AUTHORS Denefle P., Rosier-Montus M.F., Arnould-Reguigne I., Prades C.,  
 Naudin L., Lemoine C., Duverger N., Jaye M., Searfoss G.H.,  
 Remaley A., Brewer H.B. and Dean M.  
 TITLE Nucleic acids of the human abcl gene and their therapeutic and  
 diagnostic application  
 JOURNAL Patent: EP 1096012-A 17 02-MAY-2001;  
 Aventis Pharma S.A. (FR)  
 FEATURES  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 1675 a 928 c 976 g 1772 t 1 others  
 ORIGIN  
 Query Match 100.0%; Score 501; DB 6; Length 5352;  
 Best Local Similarity 100.0%; Pred. No. 3e-115;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTACAGGGCAGTGCCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 60  
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QY 481 CTGTGGCAGTAAATGCAAC 501
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Db 989 CTGTGGCAGTAAATGCAAC 1009
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RESULT 8
AX059978 Homo sapiens
LOCUS AX059978 9495 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 96 from Patent WO078970.
ACCESSION AX059978
VERSION AX059978.1 GI:12405636
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 9495)
AUTHORS Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
and Brewer,H.B.
TITLE Nucleic and proteinic acids corresponding to human gene abcl
JOURNAL Patent: WO 0078970-A 96 28-DEC-2000;
Aventis Pharma S.A. (FR)
FEATURES
source 1..9495
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2599 a 2215 c 2216 g 2564 t 1 others
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Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTTAGTTTTTACTATACCTATGTAAGTCTATTATGGAACCCCAATGACATATGGT 120
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QY 121 TTGAATCAGTCACTTTTTTTTTTTTGTTCCTGTGTTATTCATTTGGGTTGCAACAAT 180
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QY 181 AATTCATCAAGTAAATGATGCGGAGATTTATGATCAAAATCAAAAGGTAATGCATCC 240
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QY 241 TCATTCAGTAAAGCCATGCCATGCCAGAGACTGGTTTCCCGGTGACATCCATTGCTG 300
Db 7138 TCATTCAGTAAAGCCATGCCATGCCAGAGACTGGTTTCCCGGTGACATCCATTGCTG 7197
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QY 301 GCAATGAGTGGCAGAGTTATTAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCATGGT 360
Db 7198 GCAATGAGTGGCAGAGTTATTAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCATGGT 7257
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QY 361 GTGTCATGCTCAGTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG 420
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QY 421 TTGACAGATGGTGGCAGTAAACATCCTGCTTTGATTCCTCTGATAAGCTGTT 480
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QY 481 CTGTGGCAGTAAATGCAAC 501
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Db 7378 CTGTGGCAGTAAATGCAAC 7398
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RESULT 9
AX059973 Homo sapiens
LOCUS AX059973 9497 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 91 from Patent WO0078970.
ACCESSION AX059973
VERSION AX059973.1 GI:12405631
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 9497)
AUTHORS Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
and Brewer,H.B.
TITLE Nucleic and proteinic acids corresponding to human gene abcl
JOURNAL Patent: WO 0078970-A 91 28-DEC-2000;
Aventis Pharma S.A. (FR)
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/db_xref="taxon:9606"
BASE COUNT 2600 a 2115 c 2217 g 2564 t 1 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 TTGAATCAGTCACTTTTTTTTTTTTGTTCCTGTGTTATTCATTTGGGTTGCAACAAT 180
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QY 181 AATTCATCAAGTAAATGATGCGGAGATTTATGATCAAAATCAAAAGGTAATGCATCC 240
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RESULT 10
AF165281 Homo sapiens
LOCUS AF165281 9497 bp mRNA linear PRI 17-AUG-1999
DEFINITION Homo sapiens ATP cassette binding transporter 1 (ABCI) mRNA,
complete cds.
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Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7476 CTGGTGGCAGTAACATGCAAC 7496

RESULT 12  
AX127830

LOCUS AX127830 9741 bp DNA linear PAT 15-MAY-2001

DEFINITION Sequence 59 from Patent WO0130848.

ACCESSION AX127830

VERSION AX127830.1 GI:14134477

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 9741)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Nucleic acids of the human abcl gene and their therapeutic and diagnostic application

JOURNAL Patent: WO 0130848-A 59 03-MAY-2001;

FEATURES Location/Qualifiers  
source 1. .9741  
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/db\_xref="taxon:9606"

BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7e-115;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 7624 CTGGTGGCAGTAACATGCAAC 7644

RESULT 13  
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LOCUS AX139817 9741 bp DNA linear PAT 30-MAY-2001

DEFINITION Sequence 69 from Patent EP1096012.

ACCESSION AX139817

VERSION AX139817.1 GI:14275399

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 9741)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Nucleic acids of the human abcl gene and their therapeutic and diagnostic application

JOURNAL Patent: EP 1096012-A 59 02-MAY-2001;

FEATURES Location/Qualifiers  
source 1. .9741  
/organism="Homo sapiens"  
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BASE COUNT 2650 a 2180 c 2290 g 2620 t 1 others

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AX351038

LOCUS AX351038 9741 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 10 from Patent WO0183746.

ACCESSION AX351038

VERSION AX351038.1 GI:18616393

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P., Brewer, B., Duverger, N., Remaley, A., and Santamarina-Fojo, S.

TITLE Regulatory nucleic acid sequences of the abcl gene

JOURNAL Patent: WO 0183746-A 10 08-NOV-2001;

AVENTIS PHARMA S.A. (FR)

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Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 CTGGTGGCAGTAACATGCAAC 501

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Db 7624 CTGGTGGCAGTAACATGCAAC 7644

RESULT 15

AX127831

LOCUS AX127831 9854 bp DNA linear PAT 15-MAY-2001

DEFINITION Sequence 70 from Patent WO0130848.

ACCESSION AX127831

VERSION AX127831.1 GI:14134478

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Deneffe, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H., Remaley, A., Brewer, B., and Dean, M.

TITLE Nucleic acids of the human abcl gene and their therapeutic and diagnostic application

JOURNAL Patent: WO 0130848-A 70 03-MAY-2001;

AVENTIS PHARMA S.A. (FR)

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source Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 2.7e-115;

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTCAGAAAAGTTTGAAGCAACATCGGT 360

Db 7557 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTCAGAAAAGTTTGAAGCAACATCGGT 7616

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QY 421 TTGACAGAAATGGTGCCATGCGTGGCTAACATCCTGCTTTTGATTCCCTCTGATAAGCTGTT 480
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Db 7677 TTGACAGAAATGGTGCCATGCGTGGCTAACATCCTGCTTTTGATTCCCTCTGATAAGCTGTT 7736
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OM nucleic - nucleic search, using sw model

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| 23 | 479.4 | 95.7  | 5097   | 22 | AAI93913 Human stomach can  |
| 24 | 479.4 | 95.7  | 5097   | 22 | AAH18233 Human cDNA sequenc |
| 25 | 479.2 | 95.6  | 2011   | 22 | AAF24683 Nucleotide sequenc |
| 26 | 479.2 | 95.6  | 2011   | 22 | AAF24705 Nucleotide sequenc |
| 27 | 178   | 35.5  | 748    | 22 | AAF24682 Nucleotide sequenc |
| 28 | 178   | 35.5  | 748    | 22 | AAF24704 Nucleotide sequenc |
| 29 | 48.6  | 9.7   | 65     | 24 | ABN53927 Mouse spliced tran |
| 30 | 42.2  | 8.4   | 18512  | 24 | ABL32976 Human immune syste |
| 31 | 39.4  | 7.9   | 518    | 24 | ABQ15316 Oligonucleotide fo |
| 32 | 39.4  | 7.9   | 518    | 24 | ABQ15317 Oligonucleotide fo |
| 33 | 39    | 7.8   | 14307  | 24 | ABL32728 Human immune syste |
| 34 | 38.8  | 7.7   | 16602  | 24 | ABN80068 Human immune syste |
| 35 | 38.8  | 7.7   | 16602  | 24 | ABL32726 Human immune syste |
| 36 | 38.8  | 7.7   | 18357  | 23 | ABQ67083 Human angiogenesis |
| 37 | 38.4  | 7.7   | 6197   | 23 | ABL04066 Drosophila melanog |
| 38 | 37.8  | 7.5   | 1380   | 24 | ABA91277 Cryptosporidium pa |
| 39 | 37.8  | 7.5   | 30610  | 22 | ABA15643 Human nervous syst |
| 40 | 37.6  | 7.5   | 600    | 20 | AAV86185 EST clone J635. H  |
| 41 | 37.6  | 7.5   | 804    | 22 | AAI94638 Human neuroblastom |
| 42 | 37.4  | 7.5   | 5689   | 22 | AAS45384 Chemically pretrea |
| 43 | 37.4  | 7.5   | 5689   | 22 | AAS46426 Tumour suppressor  |
| 44 | 37.4  | 7.5   | 5689   | 24 | ABK28226 DNA transcription  |
| 45 | 37.4  | 7.5   | 10468  | 23 | ABL05156 Drosophila melanog |

ALIGNMENTS

RESULT 1

AAF24684

ID AAF24684 standard; DNA; 3366 BP.

XX AAF24684;

AC AAF24684;

XX 20-APR-2001 (first entry)

DT Nucleotide sequence of the 3' flanking region of the human ABC1 gene.

DE Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

KW atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

XX WO200078972-A2.

PN 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16765.

XX 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX (CVTE-) CV THERAPEUTICS INC.

XX Lawn RM, Wade D, Garvin M;

PI WPI; 2001-137812/14.

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
PT useful for the development of agents for the treatment of heart disease  
PT and other disorders associated with hypercholesterolemia and  
PT atherosclerosis -  
XX PS Disclosure: Page 146-148; 215pp; English.  
XX  
CC The present sequence represents the 3' flanking region of the human  
CC adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1  
CC resides in cell membranes and utilises ATP hydrolysis to transport a wide  
CC variety of substrates across the plasma membrane. ABC1 is a pivotal  
CC protein in the apolipoprotein-mediated mobilisation of intracellular  
CC cholesterol stores. ABC1 is defective in Tangier disease, a genetic  
CC disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1  
CC gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins  
CC are useful for developing pharmaceutical agents for the treatment of  
CC heart disease and other disorders associated with hypercholesterolemia  
CC and atherosclerosis. The genes are useful for developing screening assays  
CC to screen for compounds that regulate the expression of genes associated  
CC with cholesterol transport. The genes and proteins are also useful for  
CC are also useful as diagnostic indicators of cardiovascular disease and  
CC other disorders associated with hypercholesterolemia.  
XX  
SQ Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 3366;  
Best Local Similarity 100.0%; Pred. No. 8.1e-130;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGCCTTTGTAGCCCTATCTCTGTATGGCTCTCAAGTGAAGACTTGAA 60  
Db 174 TTACAGGGCAGTGCCTTTGTAGCCCTATCTCTGTATGGCTCTCAAGTGAAGACTTGAA 233

QY 61 TTTAGTTTTTACCTATACCTATGTAAGTCTTCTTGTATGGCTCTCAAGTGAAGACTTGAA 120  
Db 234 TTTAGTTTTTACCTATACCTATGTAAGTCTTCTTGTATGGCTCTCAAGTGAAGACTTGAA 293

QY 121 TTGAATCAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 180  
Db 294 TTGAATCAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 353

QY 181 AATTTCATCAAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 240  
Db 354 AATTTCATCAAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 413

QY 241 TCATTCATCAAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 300  
Db 414 TCATTCATCAAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 473

QY 301 GCAATGAGTGCAGAGTATAGTGCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360  
Db 474 GCAATGAGTGCAGAGTATAGTGCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 533

QY 361 GTGTCATGCTCACTTTTGTGAAGTCTCTGCTCAGAGTCTATCAACATTCATATCAG 420  
Db 534 GTGTCATGCTCACTTTTGTGAAGTCTCTGCTCAGAGTCTATCAACATTCATATCAG 593

QY 421 TTGACAGAAATGGTCCAGTGGCTTAACATCCCTGCTTTGATTCCTCTGATAAGCTGTT 480  
Db 594 TTGACAGAAATGGTCCAGTGGCTTAACATCCCTGCTTTGATTCCTCTGATAAGCTGTT 653

QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 654 CTGGTGGCAGTAACATGCAAC 674

RESULT 2  
ID AAF24706  
XX AAF24706 standard; DNA; 3366 BP.  
AC AAF24706;  
XX

DT 20-APR-2001 (first entry)  
XX Nucleotide sequence of the 3' flanking region of the human ABC1 gene.  
DE  
XX  
KW Human; adenosine triphosphate binding cassette protein 1; ABC1;  
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;  
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
KW atherosclerosis; cholesterol transport; ss.  
XX Homo sapiens.  
XX WO200078971-A2.  
XX  
PD 28-DEC-2000.  
XX  
PF 16-JUN-2000; 2000WO-US16591.  
XX  
PR 18-JUN-1999; 99US-0140264.  
PR 14-SEP-1999; 99US-0153872.  
PR 19-NOV-1999; 99US-0166573.  
XX  
XX (CVTH-) CV THERAPEUTICS INC.  
XX (UNIW) UNIV WASHINGTON.  
XX  
XX Lawn RM, Wade D, Oram JF, Garvin M;  
XX WPI; 2001-137811/14.  
XX  
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1  
PT polynucleotides and polypeptides, useful for treatment of heart disease  
PT and other disorders associated with hypercholesterolemia and  
PT atherosclerosis -  
XX  
PS Disclosure: Page 142-144; 21pp; English.  
XX  
XX The present sequence represents the 3' flanking region of the human  
CC adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1  
CC resides in cell membranes and utilises ATP hydrolysis to transport a wide  
CC variety of substrates across the plasma membrane. ABC1 is a pivotal  
CC protein in the apolipoprotein-mediated mobilisation of intracellular  
CC cholesterol stores. ABC1 is defective in Tangier disease, a genetic  
CC disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1  
CC gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins  
CC are useful for developing pharmaceutical agents for the treatment of  
CC heart disease and other disorders associated with hypercholesterolemia  
CC and atherosclerosis. The genes are useful for developing screening assays  
CC to screen for compounds that regulate the expression of genes associated  
CC with cholesterol transport. The genes and proteins are also useful for  
CC are also useful as diagnostic indicators of cardiovascular disease and  
CC other disorders associated with hypercholesterolemia.  
XX  
SQ Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 3366;  
Best Local Similarity 100.0%; Pred. No. 8.1e-130;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGCCTTTGTAGCCCTATCTCTGTATGGCTCTCAAGTGAAGACTTGAA 60  
Db 174 TTACAGGGCAGTGCCTTTGTAGCCCTATCTCTGTATGGCTCTCAAGTGAAGACTTGAA 233

QY 61 TTTAGTTTTTACCTATACCTATGTAAGTCTTCTTGTATGGCTCTCAAGTGAAGACTTGAA 120  
Db 234 TTTAGTTTTTACCTATACCTATGTAAGTCTTCTTGTATGGCTCTCAAGTGAAGACTTGAA 293

QY 121 TTGAATCAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 180  
Db 294 TTGAATCAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 353

QY 181 AATTTCATCAAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 240  
Db 354 AATTTCATCAAGTAAATCATGGCCAGGATTATGATCAAAATCAAAAGTAAATGCAATCC 413

QY 241 TCATTCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGTGACACATCCATTGGTG 300  
Db 414 TCATTCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGTGACACATCCATTGGTG 473  
QY 301 GCAATGAGTGGCCAGTATTAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCATTGGT 360  
Db 474 GCAATGAGTGGCCAGTATTAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCATTGGT 533  
QY 361 GTGTCATGCTCACTTTTGTGAAGTGCCTCTGCTCAGAGTCTATCAACATTCGAATATCAG 420  
Db 534 GTGTCATGCTCACTTTTGTGAAGTGCCTCTGCTCAGAGTCTATCAACATTCGAATATCAG 593  
QY 421 TTGACAGAATGGTGCAATGCGGTGGCTTAACATCCTGCTTTGATTCCCTCTGATAAGTGT 480  
Db 594 TTGACAGAATGGTGCAATGCGGTGGCTTAACATCCTGCTTTGATTCCCTCTGATAAGTGT 653  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 654 CTGGTGGCAGTAACATGCAAC 674  
RESULT 3  
ID AAS04049  
XX AAS04049 standard; DNA; 5352 BP.  
AC AAS04049;  
XX  
XX 12-SEP-2001 (first entry)  
DT Human ABC1 gene, partial genomic clone #15.  
DE  
DE Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Intron 1..194  
FT /tag= a  
FT /partial  
FT /note= "3' end of intron 48; this sequence is  
FT specifically claimed"  
FT /number= 48  
FT exon 195..3088  
FT /tag= b  
FT /number= 49  
FT /note= "This sequence is specifically claimed"  
FT misc\_feature 3089..5352  
FT /tag= c  
FT /note= "3' distal sequence"  
XX  
XX WC200130848-A2.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-EP10886.  
XX  
XX 26-OCT-1999; 99EP-0402668.  
PR 01-MAR-2000; 2000US-0186260.  
XX  
XX (AVET ) AVENTIS PHARMA SA.  
XX  
XX Denefle P, Rosier-Montus M, Arnould-Requigne I, Prades C, Naudin L;  
PI Lemoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;  
PI Dean M;  
XX  
XX WPI; 2001-316327/33.  
XX  
XX New human ABC1 nucleic acids and polypeptides for treating  
PT atherosclerosis, malaria and diabetes  
XX  
XX Claim 1; Page 179-182; 368pp; English.

XX The sequence represents the nucleic acid sequence of human ABC1 gene,  
CC partial genomic clone #15, comprising part of intron 48, exon 49,  
CC and 3' distal sequence. The nucleic acid sequence, primers and probes  
CC derived from the sequence, and polypeptides and vectors are useful for  
CC the prevention of atherosclerosis, in a subject affected by a dysfunction  
CC in the reverse transport of cholesterol. The polypeptide encoded by the  
CC ABC1 gene is useful for screening for an active ingredient for the  
CC prevention or treatment of a disease resulting from dysfunction in the  
CC reverse transport of cholesterol. The nucleic acids and polypeptides are  
CC also useful for treating and preventing cardiovascular and neurological  
CC pathologies, and other diseases e.g. Tangier disease, lecithin-  
CC cholesterol (LCAT) deficiency, malaria and diabetes.  
XX  
SQ Sequence 5352 BP; 1675 A; 928 C; 976 G; 1772 T; 1 other;  
Query Match 100.0%; Score 501; DB 22; Length 5352;  
Best Local Similarity 100.0%; Pred. No. 9.5e-130;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTACAGGGGCGAGTGCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGA 60  
Db 509 TTACAGGGGCGAGTGCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGA 568  
QY 61 TTTAGTCTTTTACCTATACCTATGTGAACACTTATTTGGAACCAATGGACATATGGT 120  
Db 569 TTTAGTCTTTTACCTATACCTATGTGAACACTTATTTGGAACCAATGGACATATGGT 628  
QY 121 TTGAACCTCACACTTTTTTTTTTTTTTTTCTCTGTGTATTTCTCATTTGGGTTGCAACAAT 180  
Db 629 TTGAACCTCACACTTTTTTTTTTTTTTTTCTCTGTGTATTTCTCATTTGGGTTGCAACAAT 688  
QY 181 AATTCAATCAAGTAATCATGCGCAGGATTTATGATCAAAATCAAAAGGTATGACATCC 240  
Db 689 AATTCAATCAAGTAATCATGCGCAGGATTTATGATCAAAATCAAAAGGTATGACATCC 748  
QY 241 TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGGTG 300  
Db 749 TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGGTG 808  
QY 301 GCAATGAGTGGCCAGATTTATAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCATTGGT 360  
Db 809 GCAATGAGTGGCCAGATTTATAGTCCCAAGTTTTCAGAAAGTTTGAAGCACCATTGGT 868  
QY 361 GTGTCATGCTCACTTTTGTGAAGTGCCTCTGCTCAGAGTCTATCAACATTCGAATATCAG 420  
Db 869 GTGTCATGCTCACTTTTGTGAAGTGCCTCTGCTCAGAGTCTATCAACATTCGAATATCAG 928  
QY 421 TTGACAGAATGGTGCAATGCGGTGGCTTAACATCCTGCTTTGATTCCCTCTGATAAGTGT 480  
Db 929 TTGACAGAATGGTGCAATGCGGTGGCTTAACATCCTGCTTTGATTCCCTCTGATAAGTGT 988  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 989 CTGGTGGCAGTAACATGCAAC 1009  
RESULT 4  
AAS06120  
ID AAS06120 standard; cDNA; 9741 BP.  
XX  
XX AAS06120;  
XX  
XX 12-SEP-2001 (first entry)  
XX  
XX Human ABC1 DNA sequence #1.  
XX  
XX Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;  
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.  
XX  
XX Homo sapiens.  
XX



|      |    |  |      |
|------|----|--|------|
| 61   | QY | TTTAGTGTTTTACCATACCTAATGAGAACTCTATTATGGAACCCATGACATATGGGT      | 120  |
| 7204 | Db | TTTAGTGTTTTACCATACCTAATGAGAACTCTATTATGGAACCCATGACATATGGGT      | 7263 |
| 121  | QY | TTGAACTCACAGTTTTTTTTTTTTTCTGCTGTGATCTCTCATTCGGGTGCAACAAT       | 180  |
| 7264 | Db | TTGAACTCACAGTTTTTTTTTTTTTCTGCTGTGATCTCTCATTCGGGTGCAACAAT       | 7323 |
| 181  | QY | AATTCAATCAAGTAATCATGGCCAGCGATTATGTATCAAAATCAAAAGGTAAATGCACATCC | 240  |
| 7324 | Db | AATTCAATCAAGTAATCATGGCCAGCGATTATGTATCAAAATCAAAAGGTAAATGCACATCC | 7383 |
| 241  | QY | TCATTCACTAAGCCATGCCATGCCAGCAGACTGGTTTCCCGGTGACACATCCATTGCTG    | 300  |
| 7384 | Db | TCATTCACTAAGCCATGCCATGCCAGCAGACTGGTTTCCCGGTGACACATCCATTGCTG    | 7443 |
| 301  | QY | GCAATCAGTCTGCCAGAGTATTAGTGGCAAGTTTTTCAGAAAAGTTTGAAGCACCATGGT   | 360  |
| 7444 | Db | GCAATCAGTCTGCCAGAGTATTAGTGGCAAGTTTTTCAGAAAAGTTTGAAGCACCATGGT   | 7503 |
| 361  | QY | GTGTCATGCTCACTTTTGTGAAAGTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG   | 420  |
| 7504 | Db | GTGTCATGCTCACTTTTGTGAAAGTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG   | 7563 |
| 421  | QY | TTGACAGAAATGGTCCATCGCTGGGTAAATCCTGCTTTGATTCCTCTGATAAGCTGTT     | 480  |
| 7564 | Db | TTGACAGAAATGGTCCATCGCTGGGTAAATCCTGCTTTGATTCCTCTGATAAGCTGTT     | 7623 |
| 481  | QY | CTGGTGGCAGTAACATGCAAC  | 501  |
| 7624 | Db | CTGGTGGCAGTAACATGCAAC  | 7644 |

|          |   |
|----------|---|
| RESULT 6 |   |
| AAS06121 |   |
| ID       | AAS06121 standard; cDNA; 9854 BP.                                   |
| XX       |   |
| XX       | AAS06121;   |
| XX       |   |
| XX       |   |
| DT       | 12-SEP-2001 (first entry)   |
| XX       |   |
| XX       |   |
| DE       | Human ABC1 DNA sequence #2.   |
| XX       |   |
| XX       | Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;  |
| KW       | cardiovascular; neurological; Tangier disease; LCAT deficiency;     |
| KW       | lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.      |
| XX       |   |
| OS       | Homo sapiens.   |
| XX       |   |
| XX       |   |
| Key      | Location/Qualifiers   |
| FT       | 298..7078   |
| CDS      | /*tag= a  |
| FT       | /product= "Human ABC1 protein"                                      |
| FT       |   |
| FT       |   |
| XX       |   |
| PN       | W0200130848-A2.   |
| XX       |   |
| XX       |   |
| PD       | 03-MAY-2001.  |
| XX       |   |
| XX       |   |
| PF       | 26-OCT-2000; 2000WO-EF10886.  |
| XX       |   |
| XX       |   |
| PR       | 26-OCT-1999; 99EP-0402668.  |
| PR       | 01-MAR-2000; 2000US-0186260.  |
| XX       |   |
| XX       |   |
| PA       | (AVET ) AVENTIS PHARMA SA.  |
| XX       |   |
| XX       |   |
| PI       | Denefle P, Roslier-Montus M, Arnould-Requigne I, Prades C, Naudin I |
| PI       | Leinoine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB   |
| PI       | Dean M,   |
| XX       |   |
| XX       |   |
| WPI      | 2001-316327/33.   |
| DR       | P-PSDB; AAU02176.   |
| XX       |   |
| PT       | New human ABC1 nucleic acids and polypeptides for treating          |

atherosclerosis, malaria and diabetes -  
 Claim 1; Page 209-213; 368pp; English.  
 The sequence represents the coding sequence #2 of human ABC1. The nucleic acid sequence, primers and probes derived from the ABC1 sequence, and polypeptides and vectors are useful for the prevention of atherosclerosis, in a subject affected by a dysfunction in the reverse transport of cholesterol. The polypeptide encoded by the ABC1 gene is useful for screening for an active ingredient for the prevention or treatment of a disease resulting from dysfunction in the reverse transport of cholesterol. The nucleic acids and polypeptides are also useful for treating and preventing cardiovascular and neurological pathologies, and other diseases e.g. Tangier disease, lecithin-cholesterol (LCAT) deficiency, malaria and diabetes.

|    |                       |          |   |         |            |         |              |
|----|-----------------------|----------|---|---------|------------|---------|--------------|
| XX | Sequence              | 9854 BP; | 2665 A;   | 2219 C; | 2334 G;    | 2635 T; | 1 other;     |
| XX | Query Match           | 100.0%;  | Score   | 501;    | DB         | 22;     | Length 9854; |
| PS | Best Local Similarity | 100.0%;  | Pred.   | No.     | 1.2e-129;  |         |              |
| CC | Matches               | 501;     | Conservative  | 0;      | Mismatches | 0;      | Gaps         |
| CC |                       |          |   |         |            |         |              |
| XX | QY                    | 1        | TTACAGGGCGAGTGCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA   | 60      |            |         |              |
| XX | Dd                    | 7257     | TTACAGGGCGAGTGCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA   | 7316    |            |         |              |
| XX | QY                    | 61       | TTTAGTTTTTACCATTACCTATCTGAAACTCTATTATGGAACCCCAATGCATATGGGT    | 120     |            |         |              |
| XX | Dd                    | 7317     | TTTAGTTTTTACCATTACCTATCTGAAACTCTATTATGGAACCCCAATGCATATGGGT    | 7376    |            |         |              |
| XX | QY                    | 121      | TGAACTCACACTTTTTTTTTTTTTTTTTCCTCTGTGTATTCCTCATTTGGGGTTCACAAT  | 180     |            |         |              |
| XX | Dd                    | 7377     | TGAACTCACACTTTTTTTTTTTTTTTTTCCTCTGTGTATTCCTCATTTGGGGTTCACAAT  | 7436    |            |         |              |
| XX | QY                    | 181      | AATTCAATCAAGTAATCATGCCAGCGATTATTGATCAAATAAAGAGTAAATGCATATCC   | 240     |            |         |              |
| XX | Dd                    | 7437     | AATTCAATCAAGTAATCATGCCAGCGATTATTGATCAAATAAAGAGTAAATGCATATCC   | 7496    |            |         |              |
| XX | QY                    | 241      | TCATTCACCTTAAGCCATGCCATGCCCGAGAGACTGGTTCCCGGTGACACATCCATTGGTG | 300     |            |         |              |
| XX | Dd                    | 7497     | TCATTCACCTTAAGCCATGCCATGCCCGAGAGACTGGTTCCCGGTGACACATCCATTGGTG | 7556    |            |         |              |
| XX | QY                    | 301      | GCAATGAGTGTCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAAGTTTTGAAGCACCATGGT | 360     |            |         |              |
| XX | Dd                    | 7557     | GCAATGAGTGTCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAAGTTTTGAAGCACCATGGT | 7616    |            |         |              |
| XX | QY                    | 361      | GTGTCAATGCTCACTTTTGTGAAAGTGTCTGCTCAGAGTCTATCAACATTTGAATATCAG  | 420     |            |         |              |
| XX | Dd                    | 7617     | GTGTCAATGCTCACTTTTGTGAAAGTGTCTGCTCAGAGTCTATCAACATTTGAATATCAG  | 7676    |            |         |              |
| XX | QY                    | 421      | TTGACAGAATGGTGCGATGCCGTTGGGTACATCCCTGCTTTGATTCCTCTGATAGCTGTT  | 480     |            |         |              |
| XX | Dd                    | 7677     | TTGACAGAATGGTGCGATGCCGTTGGGTACATCCCTGCTTTGATTCCTCTGATAGCTGTT  | 7736    |            |         |              |
| XX | QY                    | 481      | CTGGTGGCAGTAACATGCAAC   | 501     |            |         |              |
| XX | Dd                    | 7737     | CTGGTGGCAGTAACATGCAAC   | 7757    |            |         |              |

RESULT 7  
 AAF24680  
 ID AAF24680 standard; DNA; 10442 BP.  
 XX AC AAF24680;  
 XX DT 20-APR-2001 (first entry)  
 XX DE Nucleotide sequence of a human ABC1 polypeptide.  
 XX Human; adenosine triphosphate binding cassette protein 1; ABC1;  
 KW apolipoprotein-mediated mobilisation; cholesterol; tangier disease;  
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;  
 KW atherosclerosis; cholesterol transport; ss.

[illegible]

CC disease and other disorders associated with hypercholesterolemia and  
CC atherosclerosis. The genes are useful for developing screening assays to  
CC screen for compounds that regulate the expression of genes associated  
CC with cholesterol transport. The genes and proteins are also useful for  
CC as also useful as diagnostic indicators of cardiovascular disease and  
CC other disorders associated with hypercholesterolemia.

XX  
SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 10442;  
Best Local Similarity 100.0%; Pred. No. 1.2e-129; Indels 0; Gaps 0;  
Matches 501; Conservative 0; Mismatches 0;

QY 1 TTACAGGGCAGTGGCTTTGTAGCCTATCTTGTATGCTCTCAAGTGAAGACTTGAA 60

DB 7250 TTACAGGGCAGTGGCTTTGTAGCCTATCTTGTATGCTCTCAAGTGAAGACTTGAA 7309

QY 61 TTTAGTTTTTACCTATACCTATGTAAGTAACTCTATTATGGAACCAATGACATATGGT 120

DB 7310 TTTAGTTTTTACCTATACCTATGTAAGTAACTCTATTATGGAACCAATGACATATGGT 7369

QY 121 TTGAATCAGTCACTTTTTTTTTTTTTTTTGTCTGTATCTCAATGGGTTGCAACAAT 180

DB 7370 TTGAATCAGTCACTTTTTTTTTTTTTTTTGTCTGTATCTCAATGGGTTGCAACAAT 7429

QY 181 AATTCATCAAGTAATCATGCCAGCGATTATTCATCAAAATCAAAAGGTAATGCATCC 240

DB 7430 AATTCATCAAGTAATCATGCCAGCGATTATTCATCAAAATCAAAAGGTAATGCATCC 7489

QY 241 TCATTCACATCAAGTCACTGCCATGCCAGGAGCTGTTCCCGGTGACACATCCATTGCTG 300

DB 7490 TCATTCACATCAAGTCACTGCCATGCCAGGAGCTGTTCCCGGTGACACATCCATTGCTG 7549

QY 301 GCAATGAGTGTGCCAGGATTATAGGCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGT 360

DB 7550 GCAATGAGTGTGCCAGGATTATAGGCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGT 7609

QY 361 GTGTCATGCTCACTTTTGTGAAGCTGCTGCTCAGAGCTATCAACATTGAATATCAG 420

DB 7610 GTGTCATGCTCACTTTTGTGAAGCTGCTGCTCAGAGCTATCAACATTGAATATCAG 7669

QY 421 TTGACAGAAATGTTGCCATGCTGGCTTAACATCCTGCTTTTGAATCCCTCTGATAAGCTGT 480

DB 7670 TTGACAGAAATGTTGCCATGCTGGCTTAACATCCTGCTTTTGAATCCCTCTGATAAGCTGT 7729

QY 481 CTGGTGGCAGTACATGCAAC 501

DB 7730 CTGGTGGCAGTACATGCAAC 7750

RESULT 9

AAF24685

AC AAF24685 standard; DNA; 10474 BP.

XX AAF24685;

XX 20-APR-2001 (first entry)

DE Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;

KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;

XX atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 323..7108

FT /\*tag= a

XX /product= "defective ABC1 polypeptide"

XX WO200078972-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16765.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX (CVTH-) CV THERAPEUTICS INC.

XX Lawn RM, Wade D, Garvin M;

XX WPI; 2001-137812/14.

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,  
XX useful for the development of agents for the treatment of heart disease  
XX and other disorders associated with hypercholesterolemia and  
XX atherosclerosis -

XX Disclosure; Page 148-154; 215pp; English.

XX The present sequence encodes a human adenosine triphosphate (ATP)  
XX binding cassette protein (ABC) 1 polypeptide, and is isolated from  
XX a Tangier disease patient. ABC1 resides in cell membranes and utilizes  
XX ATP hydrolysis to transport a wide variety of substrates across the  
XX plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated  
XX mobilisation of intracellular cholesterol stores. ABC1 is defective in  
XX Tangier disease, a genetic disorder characterised by abnormal  
XX HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome  
XX 9q22-9q31. The ABC1 genes and proteins are useful for developing  
XX pharmaceutical agents for the treatment of heart disease and other  
XX disorders associated with hypercholesterolemia and atherosclerosis. The  
XX genes are useful for developing screening assays to screen for compounds  
XX that regulate the expression of genes associated with cholesterol  
XX transport. The genes and proteins are also useful for also useful  
XX as diagnostic indicators of cardiovascular disease and other disorders  
XX associated with hypercholesterolemia.

XX Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

Query Match 100.0%; Score 501; DB 22; Length 10474;  
Best Local Similarity 100.0%; Pred. No. 1.2e-129;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGGCTTTGTAGCCTATCTTGTATGCTCTCAAGTGAAGACTTGAA 60

DB 7282 TTACAGGGCAGTGGCTTTGTAGCCTATCTTGTATGCTCTCAAGTGAAGACTTGAA 7341

QY 61 TTTAGTTTTTACCTATACCTATGTAAGTAACTCTATTATGGAACCAATGCATATGGT 120

DB 7342 TTTAGTTTTTACCTATACCTATGTAAGTAACTCTATTATGGAACCAATGCATATGGT 7401

QY 121 TTGAATCAGTCACTTTTTTTTTTTTTTTTGTCTGTATCTCAATGGGTTGCAACAAT 180

DB 7402 TTGAATCAGTCACTTTTTTTTTTTTTTTTGTCTGTATCTCAATGGGTTGCAACAAT 7461

QY 181 AATTCATCAAGTAATCATGCCAGCGATTATTCATCAAAATCAAAAGGTAATGCATCC 240

DB 7462 AATTCATCAAGTAATCATGCCAGCGATTATTCATCAAAATCAAAAGGTAATGCATCC 7521

QY 241 TCATTCACATCAAGTCACTGCCATGCCAGGAGCTGTTTCCCGGTGACACATCATTCG 300

DB 7522 TCATTCACATCAAGTCACTGCCATGCCAGGAGCTGTTTCCCGGTGACACATCATTCG 7581

QY 301 GCAATGAGTGTGCCAGGTTATTAGTGCCAAAGTTTTTTCAGAAAGTTTGAAGCACCATTGGT 360

DB 7582 GCAATGAGTGTGCCAGGTTATTAGTGCCAAAGTTTTTTCAGAAAGTTTGAAGCACCATTGGT 7641

QY 361 GTGTCATGCTCACTTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 420

DB 7642 GTGTCATGCTCACTTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTGAATATCAG 7701









360 TGTGTCATGCTCAGCTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATGGAATATCA 419  
3621 TGTGTCATGCTCAGCTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATGGAATATCA 3680  
420 GTTGACAGAAATGGTCCAGTGGTGGCTTAACATCTGCTTTCATTCCTCTCTGATAGCTGT 479  
3681 GTTGACAGAAATGGTCCAGTGGTGGCTTAACATCTGCTTTCATTCCTCTCTGATAGCTGT 3740  
480 TCTGCTGGCAGTAACATGCAAC 501  
3741 TCTGCTGGCAGTAACATGCAAC 3762  
RESULT 14  
AAC69388  
ID AAC69388 standard; cDNA; 7857 BP.  
XX AAC69388;  
AC AAC69388;  
XX 29-JAN-2001 (first entry)  
DT  
XX  
DE Human ABC1 cholesterol transporter PHA-3 mutant cDNA (delta 5752-5757).  
XX  
KW Human ABC1 cholesterol transporter; chromosome 9q31;  
KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
KW Tangier disease; TD; familial HDL deficiency; PHA; polymorphism;  
KW cardiovascular disease; coronary artery disease; coronary restenosis;  
KW cerebrovascular disease; peripheral vascular disease;  
KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
KW prognosis; prophylaxis; drug screening; transgenic animal; mutant; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO20005318-A2.  
XX  
PD 21-SEP-2000.  
XX  
PF 15-MAR-2000; 2000WO-IB00532.  
XX  
PR 15-MAR-1999; 99US-0124702.  
PR 08-JUN-1999; 99US-0138048.  
PR 17-JUN-1999; 99US-0139600.  
PR 01-SEP-1999; 99US-0151977.  
XX  
XX (UYBR-) UNIV BRITISH COLUMBIA.  
PA (XENO-) XENON BIORESEARCH INC.  
XX  
XX Hayden MR, Wilson AR, Pimstone SN;  
XX  
XX WPI; 2000-587528/55.  
DR P-PSDB; AAB38107.  
XX  
PT New ABC1 polypeptide is useful for treating diseases associated with  
PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's  
PT disease and cancer -  
XX  
PS Examples; page -; 229pp; English.  
XX  
XX The invention relates to the human ABC1 cholesterol transporter protein  
XX (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is  
XX a member of the ATP-binding cassette (ABC transporter) superfamily of  
XX proteins, and plays a crucial role in cholesterol transport, particularly  
XX intracellular cholesterol trafficking in monocytes and fibroblasts, being  
XX involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
XX located on chromosome 9q31, and mutations in this gene are associated  
XX with two genetic HDL (high density lipoprotein) deficiency disorders,  
XX Tangier disease (TD) and familial HDL deficiency (PHA). These diseases  
XX are distinguishable in that TD is an autosomal recessive disorder, while  
XX PHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
XX cholesterol") in the blood correlate with a high risk of cardiovascular  
XX disease, particularly coronary artery disease, but also cerebrovascular

disease, coronary restenosis, and peripheral vascular disease.  
XX Conversely, a high level of HDL has protective effects against  
XX cardiovascular disease. The invention provides genetic constructs and  
XX transgenic cells and non-human animals comprising human ABC1 nucleic  
XX acids, and methods of gene therapy for the treatment or prevention of  
XX cardiovascular disease comprising the administration of an expression  
XX vector encoding ABC1 or an active fragment thereof. The invention also  
XX encompasses compounds which mimic ABC1 activity, compounds which  
XX stimulate ABC1 expression and methods of screening for such compounds.  
XX It further relates to methods for determining whether a patient has an  
XX increased risk for cardiovascular disease due to polymorphisms in the  
XX ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat  
XX or prevent cardiovascular disease, especially coronary artery disease,  
XX cerebrovascular disease, coronary restenosis or peripheral vascular  
XX disease. They may also be used in the treatment of diseases associated  
XX with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
XX disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
XX The invention specifically excludes proteins with the exact amino acid  
XX sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
XX acid with the exact sequence as GenBank Accession No: AF012376.1. The  
XX present sequence represents cDNA encoding a mutant human ABC1 cholesterol  
XX transporter associated with an altered cholesterol level and therefore an  
XX altered risk of cardiovascular disease.  
XX Note: The present sequence is not shown in the specification, but is  
XX derived from the native human ABC1 cDNA shown on pages 157-160.  
XX  
SQ Sequence 7857 BP; 2011 A; 1860 C; 2008 G; 1977 T; 1 other;  
Query Match 97.88; Score 490; DB 21; Length 7857;  
Best Local Similarity 99.88; Pred. No. 1.3e-126;  
Matches 501; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 TTACAGGGCGAGTGGCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 60  
DB 7031 TTACAGGGCGAGTGGCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 7090  
QY 61 TTTAGTCTTTTACCTATACCTATGTAACCTCTATTATGGAACCAATGGACATATGGT 120  
DB 7091 TTTAGTCTTTTACCTATACCTATGTAACCTCTATTATGGAACCAATGGACATATGGT 7150  
QY 121 TTGAACCTCACAC-TTTTTTTTTTTTTTTTGTCTCTGTATTTCTCATTTGGGTTGCAACAA 179  
DB 7151 TTGAACCTCACACTTTTTTTTTTTTTTTTGTCTCTGTATTTCTCATTTGGGTTGCAACAA 7210  
QY 180 TAATTCAATCAAGTAATCATGCGCCAGCGATTTATGATCAAAATCAAAAGGTTATGCAATC 239  
DB 7211 TAATTCAATCAAGTAATCATGCGCCAGCGATTTATGATCAAAATCAAAAGGTTATGCAATC 7270  
QY 240 CTCATTCATCAAGCCATGCCATGCCAGGAGACTGTTTCCCGGTGACACATCCATTTGCT 299  
DB 7271 CTCATTCATCAAGCCATGCCATGCCAGGAGACTGTTTCCCGGTGACACATCCATTTGCT 7330  
QY 300 GGCAATGAGTGTGCCAGAGTTATTAGTGCCTAGTTTTCAGAAAGTTTGAACACCATGG 359  
DB 7331 GGCAATGAGTGTGCCAGAGTTATTAGTGCCTAGTTTTCAGAAAGTTTGAACACCATGG 7390  
QY 360 TGTGTCATGCTCAGCTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATGGAATATCA 419  
DB 7391 TGTGTCATGCTCAGCTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCAACATGGAATATCA 7450  
QY 420 GTTGACAGAAATGGTCCAGTGGTGGCTTAACATCTGCTTTCATTCCTCTCTGATAGCTGT 479  
DB 7451 GTTGACAGAAATGGTCCAGTGGTGGCTTAACATCTGCTTTCATTCCTCTCTGATAGCTGT 7510  
QY 480 TCTGCTGGCAGTAACATGCAAC 501  
DB 7511 TCTGCTGGCAGTAACATGCAAC 7532  
RESULT 15  
AAF83826  
ID AAF83826 standard; DNA; 7860 BP.  
XX

|    |  |
|----|--|
| AC | AA83826;   |
| XX |  |
| DT | 06-AUG-2001 (first entry)  |
| XX |  |
| DE | Human ABC1 nucleotide sequence.  |
| XX |  |
| KW | ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;      |
| KW | LDL; ds.   |
| XX |  |
| OS | Homo sapiens.  |
| XX |  |
| FT | Key  |
| FT | CDS  |
| FT | Location/Qualifiers  |
| FT | 75..3341   |
| FT | /*tag= a   |
| FT | /product= "partial ABC1 protein"   |
| FT | /note= "the coding sequence continues beyond nucleotide                  |
| FT | 3341, possibly till position 6860 as identified                          |
| FT | by translating the present sequence; part of the                         |
| FT | corresponding protein is missing and nucleotide                          |
| FT | 3341 corresponds to the last amino acid residue                          |
| FT | (position 1089) as indicated in the                                      |
| FT | specification"   |
| XX |  |
| FN | W0200132184-A2.  |
| XX |  |
| XX | 10-MAY-2001.   |
| XX |  |
| XX | 01-NOV-2000; 2000WO-US30109.   |
| XX |  |
| XX | 01-NOV-1999; 99US-0162803.   |
| PR |  |
| PR | 30-JUN-2000; 2000US-0215564.   |
| XX |  |
| XX | (WISC ) WISCONSIN ALUMNI RES FOUND.                                      |
| PA |  |
| XX |  |
| PI | Attie AD, Cook M, Gray-Keller MP, Hayden MR, Pimstone S;                 |
| PI | Brooks-Wilson A;   |
| XX |  |
| DR | WPI; 2001-335779/35.   |
| DR | P-PSDB; AAB62691.  |
| XX |  |
| PT | New method for inhibiting cholesterol uptake in the gut comprises        |
| PT | administration of an inhibitor of an ABC1 protein                        |
| XX |  |
| PS | Disclosure; Page 34-36; 41pp; English.                                   |
| XX |  |
| CC | The invention relates to a new method for inhibiting cholesterol uptake  |
| CC | in the gut that comprises administration of an inhibitor of an ABC1      |
| CC | protein. The method is useful for: lowering levels of LDL (low density   |
| CC | lipoprotein) cholesterol by reducing the activity of ABC1 protein in the |
| CC | intestinal cells and the abundance of the ABC1 protein in the individual |
| CC | by inhibiting the activity of the protein; identifying drugs that can    |
| CC | lower serum cholesterol and LDL levels comprises assaying the drug to    |
| CC | test if it can bind to an ABC1 protein; testing LDL cholesterol lowering |
| CC | agents; and for modulation of ABC1 biological activity. The present      |
| CC | sequence represents a human ABC1 nucleotide sequence.                    |
| XX |  |
| SQ | Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;               |
|    |  |
|    | Query Match 97.8%; Score 490; DB 22; Length 7860;                        |
|    | Best Local Similarity 99.8%; Pred. No. 1.3e-126;                         |
|    | Matches 501; Conservative 0; Mismatches 0; Indels 1; Gaps 1;             |
| QY | 1 TTACAGGGGCAGTGCTTTGTAGCCATGCTCTTGTATGGCTCTCAAGTGAAGACATTGAA 60         |
| Db | 7034 TTACAGGGGCAGTGCTTTGTAGCCATGCTCTTGTATGGCTCTCAAGTGAAGACATTGAA 7093    |
| QY | 61 TTAGTATTTTACCTATACCTATGTGAACACTCTATTATGGAACCAATGGACATATGGGT 120       |
| Db | 7094 TTAGTATTTTACCTATACCTATGTGAACACTCTATTATGGAACCAATGGACATATGGGT 7153    |
| QY | 121 TTGAAGTACAC-TTTTTTTTTTTTTTTTGGTTCCTGTTATTCATTTGGGGTTGCAACA 179       |
| Db | 7154 TTGAAGTACACTTTTTTTTTTTTTTTTGGTTCCTGTTATTCATTTGGGGTTGCAACA 7213      |

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13.777 seconds  
(without alignments)  
11152.306 Million cell updates/sec

Title: US-09-595-526C-1\_COPY\_7250\_7750  
Perfect score: 501  
Sequence: 1 ttacaggggcagtgcttgg.....tgggtggcagtaacatgaac 501

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\*

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.\*  
1: /cgn2.6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2.6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2.6/ptodata/1/ina/5A\_COMB.seq.\*  
4: /cgn2.6/ptodata/1/ina/5B\_COMB.seq.\*  
5: /cgn2.6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description        |
|------------|-------|---------------|--------|-------|--------------------|
| C 1        | 35    | 7.0           | 4010   | 5     | PCT-US94-07297-40  |
| C 2        | 34.8  | 6.9           | 2378   | 4     | US-08-802-805D-20  |
| C 3        | 34.8  | 6.9           | 169998 | 4     | US-09-676-610B-24  |
| C 4        | 34.6  | 6.9           | 945    | 4     | US-09-134-001C-415 |
| C 5        | 34.4  | 6.9           | 748    | 1     | US-08-361-467B-3   |
| C 6        | 34.4  | 6.9           | 748    | 1     | US-08-484-332C-3   |
| C 7        | 34.2  | 6.8           | 681    | 4     | US-09-134-001C-741 |
| C 8        | 34    | 6.8           | 7351   | 1     | US-08-224-391-83   |
| C 9        | 34    | 6.8           | 7351   | 1     | US-08-484-304-83   |
| C 10       | 34    | 6.8           | 7351   | 2     | US-08-184-009-127  |
| C 11       | 34    | 6.8           | 7351   | 2     | US-08-566-398-39   |
| C 12       | 34    | 6.8           | 7351   | 2     | US-08-458-356-127  |
| C 13       | 34    | 6.8           | 7351   | 2     | US-08-658-665-39   |
| C 14       | 34    | 6.8           | 7351   | 4     | US-08-796-101-3    |
| C 15       | 34    | 6.8           | 7351   | 4     | US-08-460-736-127  |
| C 16       | 34    | 6.8           | 7351   | 4     | US-09-085-273-39   |
| C 17       | 33.8  | 6.7           | 4526   | 1     | US-07-855-412B-4   |
| C 18       | 33.8  | 6.7           | 4526   | 2     | US-08-308-887A-4   |
| C 19       | 33.8  | 6.7           | 4526   | 3     | US-08-881-094-4    |
| C 20       | 33.4  | 6.7           | 8920   | 2     | US-08-446-855A-1   |
| C 21       | 33.4  | 6.7           | 8920   | 4     | US-09-150-741-1    |
| C 22       | 33    | 6.6           | 2193   | 4     | US-09-427-261-2    |
| C 23       | 33    | 6.6           | 2193   | 4     | US-09-427-261-3    |
| C 24       | 32.8  | 6.5           | 609    | 1     | US-08-268-072-2    |
| C 25       | 32.8  | 6.5           | 609    | 4     | US-08-690-721-2    |
| C 26       | 32.4  | 6.5           | 1651   | 4     | US-09-465-558-49   |
| C 27       | 32.2  | 6.4           | 114    | 1     | US-08-120-827-99   |
| C 28       | 32.2  | 6.4           | 114    | 1     | US-08-478-675-99   |
| C 29       | 32    | 6.4           | 740    | 2     | US-08-713-000-8    |
| C 30       | 32    | 6.4           | 740    | 2     | US-08-975-316-8    |
| C 31       | 32    | 6.4           | 740    | 4     | US-09-211-710-8    |
| C 32       | 32    | 6.4           | 740    | 4     | US-09-615-192A-8   |
| C 33       | 32    | 6.4           | 741    | 2     | US-08-975-316-58   |
| C 34       | 32    | 6.4           | 741    | 4     | US-09-615-192A-58  |
| C 35       | 32    | 6.4           | 788    | 4     | US-09-615-192A-96  |
| C 36       | 32    | 6.4           | 3167   | 4     | US-09-276-531-132  |
| C 37       | 32    | 6.4           | 4668   | 4     | US-09-045-301-1    |
| C 38       | 31.8  | 6.3           | 2196   | 1     | US-08-090-523-29   |
| C 39       | 31.8  | 6.3           | 2196   | 1     | US-08-334-639-1    |
| C 40       | 31.8  | 6.3           | 2196   | 1     | US-08-398-627-29   |
| C 41       | 31.8  | 6.3           | 2196   | 1     | US-08-406-858-24   |
| C 42       | 31.8  | 6.3           | 2196   | 5     | PCT-US94-05275-24  |
| C 43       | 31.8  | 6.3           | 2700   | 3     | US-09-315-861-1    |
| C 44       | 31.8  | 6.3           | 2700   | 4     | US-09-398-395A-43  |
| C 45       | 31.8  | 6.3           | 3083   | 2     | US-08-480-994-36   |

#### ALIGNMENTS

#### RESULT 1

PCT-US94-07297-40/C  
; Sequence 40, Application PC/TUS9407297

; GENERAL INFORMATION:

; APPLICANT: Arai, Naoko

; APPLICANT: Masuda, Esteban S.

; APPLICANT: Tokumitsu, Hiroshi

; TITLE OF INVENTION: PURIFIED COMPONENTS OF MAMMALIAN

; TITLE OF INVENTION: TRANSCRIPTION REGULATION COMPLEXES, AND ANALOGS

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John H. C. Blasdale, Schering-Plough Corporation, M-3-W

; STREET: One Giralda Farms

; CITY: Madison

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07940-1000

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh Iicx

; OPERATING SYSTEM: System Software 7.1

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/07297

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/222,626

; FILING DATE: 04-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/148,061

; FILING DATE: 05-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/113,971

; FILING DATE: 30-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/099,998

; FILING DATE: 30-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/088,483

; FILING DATE: 06-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Blasdale, John H. C.

; REGISTRATION NUMBER: 31,895

; REFERENCE/DOCKET NUMBER: DX0392K4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-822-7398

; TELEFAX: 201-822-7039

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

Sequence 99, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 8, Appl  
Sequence 58, Appl  
Sequence 58, Appl  
Sequence 96, Appl  
Sequence 132, Appl  
Sequence 29, Appl  
Sequence 1, Appl  
Sequence 29, Appl  
Sequence 29, Appl  
Sequence 24, Appl  
Sequence 1, Appl  
Sequence 43, Appl  
Sequence 36, Appl

```

; LENGTH: 4010 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 304..3531
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: replace(1756..1758, "gta")
;   FEATURE:
;   NAME/KEY: unsure
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;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: replace(1756..1758, "gga")
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: replace(3090..3092, "agt")
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: replace(3090..3092, "aga")
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: replace(3090..3092, "agg")
;
; PCT-US94-07297-40
;
; Query Match 7.0%; Score 35; DB 5; Length 4010;
; Best Local Similarity 51.6%; Pred. No. 0.6;
; Matches 80; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
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; QY 133 TTTTCTTTTCTTCTGTCGTCATTCATTCGTTGCGGTTGCAACAATAATTCATCAAGT 192
; DB 3994 TTTTCTTTTCTTCTGTCGTCATTCATTCGTTGCGGTTGCAACAATAATTCATCAAGT 192
;
; QY 193 AATCATGCCAGCGATTATTCATCAAAATCAAAAGTAAATGCACATCCTCATTCCTCAAGT 252
; DB 3934 GTTCCTATTTAAATATATCAATAAATCAAGGCGCCCTTCAATGACCAATAAGCAGT 3875
;
; QY 253 CCATGCCATGCCAGGACTGTTCCGGTGAC 287
; DB 3874 ACAATCACCACCTCCTAGTTAAGTAACAGGTCAC 3840
;
; RESULT 2
; US-08-805D-20/C
; Sequence 20, Application US/0802805D
; Patent No. 6372453
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,805D
; FILING DATE: 18-Feb-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PHD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: PI086
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/352-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2378 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
; US-08-802-805D-20
;
; Query Match 6.9%; Score 34.8; DB 4; Length 2378;
; Best Local Similarity 53.7%; Pred. No. 0.56;
; Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
;
; QY 133 TTTTCTTTTCTTCTGTCGTCATTCATTCGTTGCGGTTGCAACAATAATTCATCAAGT 192
; DB 2289 TTTTCTTTTCTTCTGTCGTCATTCATTCGTTGCGGTTGCAACAATAATTCATCAAGT 192
;
; QY 193 AATCATGCCAGCGATTATTCATCAAAATCAAAAGTAAATGCACATCCTCATTCCTCAAGT 252
; DB 2229 GCTACATTCAGCTTCTCCTCACTCAAGCAAGCTCAGAGAGTCCCATCAACAATCCGGGAG 2170
;
; QY 253 CCATGCCATGCCAGGCGCA 266
; DB 2169 CTGTGCCAGGCGCA 2156
;
; RESULT 3
; US-09-676-610B-24
; Sequence 24, Application US/09676610B
; Patent No. 6444465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RFS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 24
; LENGTH: 169998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1208)...(1472)
; NAME/KEY: intron
; LOCATION: (1473)...(124390)
; NAME/KEY: exon
; LOCATION: (124391)...(124544)
; NAME/KEY: intron
; LOCATION: (124545)...(125409)
; NAME/KEY: exon
; LOCATION: (125410)...(125595)
; NAME/KEY: intron
; LOCATION: (125596)...(128711)
; NAME/KEY: exon
; LOCATION: (128712)...(128848)
; NAME/KEY: intron
; LOCATION: (128849)...(133400)
; NAME/KEY: exon
; LOCATION: (133401)...(133469)
; NAME/KEY: intron
; LOCATION: (133470)...(134652)
; NAME/KEY: exon
; LOCATION: (134653)...(134773)
; NAME/KEY: intron
; LOCATION: (134774)...(136116)
; NAME/KEY: exon
; LOCATION: (136117)...(136261)
; NAME/KEY: intron
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; FILING DATE: 01-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 89 402 224.3
; FILING DATE: 04-AUG-1989

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DB 202 TTTTATTAAACCTTTTGGCTATTCTTTTATTATTCGCT  
QY 175 AACCAATAATTCATCAAGTAATCATGGCCAGCGA



QY 235 ACATCCTCATT 245  
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DB 82 ACATTATTAT 72

RESULT 8  
US-08-224-391-83/c  
; Sequence 83, Application US/08224391  
; Patent No. 5744140  
; GENERAL INFORMATION:  
; APPLICANT: Paoletti, Enzo  
; APPLICANT: Pincus, Steven E.  
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; ADDRESSEE: c/o William S. Frommer  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,391  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/729,800  
; FILING DATE: 17-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer, William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2340  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7351 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-224-391-83

Query Match 6.8%; Score 34; DB 1; Length 7351;  
Best Local Similarity 54.9%; Pred. No. 1.5;  
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 26 TATGCTCTGATGGCTCAAGTGAAGACTGAAATTTAGTTTACCTATACCTATGT 85  
|||||  
DB 2637 TATATCGTATAAATATGTCAGATGAATGAATTTATTAAAGGGTTATACCTTTAAGTATGT 2578  
|||||

QY 86 GAACTCTATTATGGAACCAATGACATATGGGTTTGAACACACATTTTCTATAGTTT 145  
|||||  
DB 2577 TTATCTCTTTAATAACAATCATCTTTAATTAATTTGAATATATCATTTTCTATAGTTT 2518  
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QY 146 TT 147  
||  
DB 2517 TT 2516

RESULT 9  
US-08-484-304-83/c  
; Sequence 83, Application US/08484304  
; Patent No. 5744141  
; GENERAL INFORMATION:  
; APPLICANT: Paoletti, Enzo  
; APPLICANT: Pincus, Steven E.

; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; ADDRESSEE: c/o William S. Frommer  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,304  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,391  
; FILING DATE:  
; APPLICATION NUMBER: US 07/729,800  
; FILING DATE: 17-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer, William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2340  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7351 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-484-304-83

Query Match 6.8%; Score 34; DB 1; Length 7351;  
Best Local Similarity 54.9%; Pred. No. 1.5;  
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 26 TATGCTCTGATGGCTCAAGTGAAGACTGAAATTTAGTTTACCTATACCTATGT 85  
|||||  
DB 2637 TATATCGTATAAATATGTCAGATGAATGAATTTATTAAAGGGTTATACCTTTAAGTATGT 2578  
|||||

QY 86 GAACTCTATTATGGAACCAATGACATATGGGTTTGAACACACATTTTCTATAGTTT 145  
|||||  
DB 2577 TTATCTCTTTAATAACAATCATCTTTAATTAATTTGAATATATCATTTTCTATAGTTT 2518  
|||||

QY 146 TT 147  
||  
DB 2517 TT 2516

RESULT 10  
US-08-184-009-127/c  
; Sequence 127, Application US/08184009  
; Patent No. 5833975  
; GENERAL INFORMATION:  
; APPLICANT: Paoletti, Enzo  
; APPLICANT: Tartaglia, James  
; APPLICANT: Cox, William I.  
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY  
; NUMBER OF SEQUENCES: 217  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Safford  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/184,009  
FILING DATE: 19-JAN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
TELEX: 425066CURTMS  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7351 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-184-009-127

Query Match 6.8%; Score 34; DB 2; Length 7351;  
Best Local Similarity 54.9%; Pred. No. 1.5;  
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 26 TATGCTGTGATGGCTCTCAAGTGAAGAGCTTGAATTTAGTTTACCTATACCTATGT 85  
DB 2637 TATATCGTATAAATATGTCAGATGAATGAATTTATTAAGGGTTATCTTTAAGTATGT 2578  
QY 86 GAAACTCTATTATGGAACCAACCAATGGACATATGGGTTTGAACCTACACACTTTTTTTTTT 145  
DB 2577 TTATCTCTTTAATACATCATCTTTAATTAATTGAATATACATTTTCTATAGTTT 2518  
QY 146 TT 147  
DB 2517 TT 2516

RESULT 11  
US-08-566-398-39/c  
Sequence 39, Application US/08566398  
Patent No. 5858373  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Gettig, Russell  
TITLE OF INVENTION: RECOMBINANT POXVIRUS - FELINE INFECTIOUS  
TITLE OF INVENTION: PERITONITIS VIRUS, COMPOSITIONS THEREOF, AND METHODS FOR  
TITLE OF INVENTION: MAKING AND USING THEM  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford, P.C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/566,398  
FILING DATE: 01-DEC-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2880  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7351 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-566-398-39

Query Match 6.8%; Score 34; DB 2; Length 7351;  
Best Local Similarity 54.9%; Pred. No. 1.5;  
Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 26 TATGCTGTGATGGCTCTCAAGTGAAGAGCTTGAATTTAGTTTACCTATACCTATGT 85  
DB 2637 TATATCGTATAAATATGTCAGATGAATGAATTTATTAAGGGTTATCTTTAAGTATGT 2578  
QY 86 GAAACTCTATTATGGAACCAACCAATGGACATATGGGTTTGAACCTACACACTTTTTTTTTT 145  
DB 2577 TTATCTCTTTAATACATCATCTTTAATTAATTGAATATACATTTTCTATAGTTT 2518  
QY 146 TT 147  
DB 2517 TT 2516

RESULT 12  
US-08-458-356-127/c  
Sequence 127, Application US/08458356  
Patent No. 5942235  
GENERAL INFORMATION:  
APPLICANT: Paoletti, Enzo  
APPLICANT: Tartaglia, James  
APPLICANT: Cox, William I.  
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 217  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Curtis, Morris & Safford  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,356  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/184,009  
FILING DATE: 19-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer, William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 840-3333  
TELEFAX: (212) 840-0712  
TELEX: 425066CURTMS  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7351 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
US-08-458-356-127

Query Match 6.8%; Score 34; DB 2; Length 7351;

Best Local Similarity 54.9%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;

Matches 67; Conservative 0;

QY 26 TATGTCCTGATGGCTCTCAAGTGAAGACTTGAATTTAGTTTTTACCTATACCTATGT 85

Db 2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAGGGTTATACCTTTTAAAGTATGT 2578

QY 86 GAAACTCTATTATGGGAACCAATGGACATATGGTTTGAAGTTCACACTTTTTTTTTTTT 145

Db 2577 TTATCTCTTTAATAACAATCATCTTTAATTAATTTGAATATATCATATTATTTCTATAGTTT 2518

QY 146 TT 147

Db 2517 TT 2516

RESULT 13

US-08-658-665-39/c

Sequence 39, Application US/08658665

Patent No. 5997878

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Pincus, Steven E.

APPLICANT: Cox, William I.

APPLICANT: Kauffman, Elizabeth K.

TITLE OF INVENTION: Recombinant Poxvirus - Cytomegalovirus,

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford, P.C.

STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/658,665

FILING DATE: 05-JUN-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Frommer Esq., William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2720.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)840-3333

TELEFAX: (212)840-0712

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 7351 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-658-665-39

Query Match 6.8%; Score 34; DB 2; Length 7351;

Best Local Similarity 54.9%; Pred. No. 1.5;

Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 26 TATGTCCTGATGGCTCTCAAGTGAAGACTTGAATTTAGTTTTTACCTATACCTATGT 85

Db 2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAGGGTTATACCTTTTAAAGTATGT 2578

QY 86 GAAACTCTATTATGGGAACCAATGGACATATGGGTTTGAAGTTCACACTTTTTTTTTTTT 145

Db 2577 TTATCTCTTTAATAACAATCATCTTTAATTAATTTGAATATATCATATTATTTCTATAGTTT 2518

QY 146 TT 147

Db 2517 TT 2516

RESULT 15

US-08-460-736-127/c

Db 2577 TTATCTCTTTAATAACAATCATCTTTAATTAATTTGAATATATCATATTATTTCTATAGTTT 2518

QY 146 TT 147

Db 2517 TT 2516

RESULT 14

US-08-796-101-3/c

Sequence 3, Application US/08796101

Patent No. 6183752

GENERAL INFORMATION:

APPLICANT: EPSTEIN, STEPHEN E.

APPLICANT: FINKEL, TOREN

APPLICANT: SPEIR, EDITH

APPLICANT: ZHOU, YI FU

APPLICANT: ZHU, JIANHUI

APPLICANT: ERDILE, LORNE

APPLICANT: PINCUS, STEVEN

TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,

TITLE OF INVENTION: PROPHYLAXIS AND THERAPY

NUMBER OF SEQUENCES: 184

CORRESPONDENCE ADDRESS:

ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.

STREET: 530 FIFTH AVENUE

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/796,101

FILING DATE: 05-FEB-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: KOWALSKI, THOMAS J.

REGISTRATION NUMBER: 32,147

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 764-5574

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 7351 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-796-101-3

Query Match 6.8%; Score 34; DB 4; Length 7351;

Best Local Similarity 54.9%; Pred. No. 1.5;

Matches 67; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 26 TATGTCCTGATGGCTCTCAAGTGAAGACTTGAATTTAGTTTTTACCTATACCTATGT 85

Db 2637 TATATCGTATAAATATGTCAGATGAATGAAATTTATTAGGGTTATACCTTTTAAAGTATGT 2578

QY 86 GAAACTCTATTATGGGAACCAATGGACATATGGGTTTGAAGTTCACACTTTTTTTTTTTT 145

Db 2577 TTATCTCTTTAATAACAATCATCTTTAATTAATTTGAATATATCATATTATTTCTATAGTTT 2518

QY 146 TT 147

Db 2517 TT 2516

RESULT 15

US-08-460-736-127/c

Search completed: April 3, 2003, 14:25:36  
Job time : 160.777 secs



QY 121 TTGAACACACACTTTTTTTTTTTTTTTTTTTTGTCTGTTATCTCTCATTTGGGGTGCACAAAT 180  
Db 435 TTGAACACACACTTTTTTTTTTTTTTTTTTTTGTCTGTTATCTCTCATTTGGGGTGCACAAAT 494  
QY 181 AATTCAATCAAGTAATCATGCGCCAGCAGATTTATGATCAAAATCAAAAGGTAATGCACATCC 240  
Db 495 AATTCAATCAAGTAATCATGCGCCAGCAGATTTATGATCAAAATCAAAAGGTAATGCACATCC 554  
QY 241 TCATTCAATCAAGCAGTCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300  
Db 555 TCATTCAATCAAGCAGTCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614  
QY 301 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTTCAGAAAAGTTTGAAGCACCATTGGT 360  
Db 615 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTTCAGAAAAGTTTGAAGCACCATTGGT 674  
QY 361 GTGTCATGCTCACTTTTGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 420  
Db 675 GTGTCATGCTCACTTTTGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 734  
QY 421 TTGACAGAAATGGTGGCAGTGGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 480  
Db 735 TTGACAGAAATGGTGGCAGTGGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 794  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 795 CTGGTGGCAGTAACATGCAAC 815

## RESULT 2

US-09-984-827-86  
; Sequence 86, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984, 827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 86  
; LENGTH: 2894  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (180)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-86

Query Match 100.0%; Score 501; DB 9; Length 2894;  
Best Local Similarity 100.0%; Pred. No. 8.5e-135;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGCCTTTGAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 60  
Db 315 TTACAGGGCAGTGCCTTTGAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 374  
QY 61 TTTAGTTTTTACCTATACCTATGTAAGTCTATTTATGAAACCAATGACATATGGT 120  
Db 375 TTTAGTTTTTACCTATACCTATGTAAGTCTATTTATGAAACCAATGACATATGGT 434

QY 121 TTGAACACACACTTTTTTTTTTTTTTTTTTTTGTCTGTTATCTCTCATTTGGGGTGCACAAAT 180  
Db 435 TTGAACACACACTTTTTTTTTTTTTTTTTTTTGTCTGTTATCTCTCATTTGGGGTGCACAAAT 494  
QY 181 AATTCAATCAAGTAATCATGCGCCAGCAGATTTATGATCAAAATCAAAAGGTAATGCACATCC 240  
Db 495 AATTCAATCAAGTAATCATGCGCCAGCAGATTTATGATCAAAATCAAAAGGTAATGCACATCC 554  
QY 241 TCATTCAATCAAGCAGTCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 300  
Db 555 TCATTCAATCAAGCAGTCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTG 614  
QY 301 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTTCAGAAAAGTTTGAAGCACCATTGGT 360  
Db 615 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTTCAGAAAAGTTTGAAGCACCATTGGT 674  
QY 361 GTGTCATGCTCACTTTTGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 420  
Db 675 GTGTCATGCTCACTTTTGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 734  
QY 421 TTGACAGAAATGGTGGCAGTGGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 480  
Db 735 TTGACAGAAATGGTGGCAGTGGTGAAGCTGCTCTCAGAGTCTATCAAGATTAATCAATCAG 794  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 795 CTGGTGGCAGTAACATGCAAC 815

## RESULT 3

US-09-984-827-87  
; Sequence 87, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFFLE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984, 827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 87  
; LENGTH: 2894  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (180)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-87

Query Match 100.0%; Score 501; DB 9; Length 2894;  
Best Local Similarity 100.0%; Pred. No. 8.5e-135;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGCCTTTGAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 60  
Db 315 TTACAGGGCAGTGCCTTTGAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 374  
QY 61 TTTAGTTTTTACCTATACCTATGTAAGTCTATTTATGAAACCAATGACATATGGT 120  
Db 375 TTTAGTTTTTACCTATACCTATGTAAGTCTATTTATGAAACCAATGACATATGGT 434  
QY 121 TTGAACACACACTTTTTTTTTTTTTTTTTTTTGTCTGTTATCTCTCATTTGGGGTGCACAAAT 180

|    |     |   |     |
|----|-----|---|-----|
| Db | 435 | TTGAACTCACACITTTTTTTTTTTTTTTGTTCCGTGTATCTCTCATTTGGGGTTGCCAACAT  | 494 |
| Qy | 181 | AATTCATCAAGTAAATCATGCCGACGGATTAATGATCAAAATCAAAAGGTAATGCCACATCC  | 240 |
| Db | 495 | AATTCATCAAGTAAATCATGCCGACGGATTAATGATCAAAATCAAAAGGTAATGCCACATCC  | 554 |
| Qy | 241 | TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTTCCGGGTGACACATCCATTGGTG     | 300 |
| Db | 555 | TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTTCCGGGTGACACATCCATTGGTG     | 614 |
| Qy | 301 | GCAATGAGTGTGCCAGAGATTATTAGTGCCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGGT | 360 |
| Db | 615 | GCAATGAGTGTGCCAGAGATTATTAGTGCCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGGT | 674 |
| Qy | 361 | GTGTCATGCTCACTTTTGTGAAAGCTGCTGTCTCAGAGTCTATCAACATTGTAATATCAG    | 420 |
| Db | 675 | GTGTCATGCTCACTTTTGTGAAAGCTGCTGTCTCAGAGTCTATCAACATTGTAATATCAG    | 734 |
| Qy | 421 | TTGACAGAAATGGTGCCATGGTGGCTAACATCTCGTTTGATTCCCTCTCATGAAGCTGTT    | 480 |
| Db | 735 | TTGACAGAAATGGTGCCATGGTGGCTAACATCTCGTTTGATTCCCTCTCATGAAGCTGTT    | 794 |
| Qy | 481 | CTGTGGCAGTAACATGCAAC  | 501 |
| Db | 795 | CTGTGGCAGTAACATGCAAC  | 815 |

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RESULT 5
US-09-984-827-89
; Sequence 89, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTIUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-000000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-89

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|    |                       |   |              |               |            |    |        |         |
|----|-----------------------|---|--------------|---------------|------------|----|--------|---------|
|    | Query Match           | 100.0%  | Score        | 501;          | DB         | 9; | Length | 2894;   |
|    | Best Local Similarity | 100.0%;   | Pred.        | No. 8.5e-135; |            |    |        |         |
|    | Matches               | 501;  | Conservative | 0;            | Mismatches | 0; | Indels | 0; Gaps |
| QY | 1                     | TTACAGGGCAGTGCCTTTGTAGCCATGTCCTGTATGCGCTCTCAAGTGAAAGACTTGAA     | 60           |               |            |    |        |         |
|    |                       |   |              |               |            |    |        |         |
| Dd | 315                   | TTACAGGGCAGTGCCTTTGTAGCCATGTCCTGTATGCGCTCTCAAGTGAAAGACTTGAA     | 374          |               |            |    |        |         |
|    |                       |   |              |               |            |    |        |         |
| QY | 61                    | TTTAGTTTTTACCCTATACCTATGTCGAAACTCTATTATGGAACCCAATGGACATATGGGT   | 120          |               |            |    |        |         |
|    |                       |   |              |               |            |    |        |         |
| Dd | 375                   | TTTAGTTTTTACCCTATACCTATGTAACCTCTATTATGGAACCCAATGGACATATGGGT     | 434          |               |            |    |        |         |
|    |                       |   |              |               |            |    |        |         |
| QY | 121                   | TGAACTCACACTTTTTTTTTTTTTTTTTTTTGGTCTGTGTAATTCATNTGGGGTTGCCAACAT | 180          |               |            |    |        |         |
|    |                       |   |              |               |            |    |        |         |
| Db | 435                   | TGAACTCACACTTTTTTTTTTTTTTTTTTTTGGTCTGTGTAATTCATNTGGGGTTGCCAACAT | 494          |               |            |    |        |         |
|    |                       |   |              |               |            |    |        |         |

|  |      |   |     |            |                   |
|--|------|---|-----|------------|-------------------|
| Best bound similarity 100.0%, Plo. NO. 8.5E-195; |      |   |     |            |                   |
| Matches  | 501; | Conservative  | 0;  | Mismatches | 0; Indels 0; Gaps |
| QY   | 1    | TTACAGGGGCAGTGCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA     | 60  |            |                   |
|  |      |   |     |            |                   |
| Db   | 315  | TTACAGGGGCAGTGCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA     | 374 |            |                   |
|  |      |   |     |            |                   |
| QY   | 61   | TTTAGTTTTTACCTATACCTATGTGAAGACTCTATTATGGAACCCCAATGGACATATGGGT   | 120 |            |                   |
|  |      |   |     |            |                   |
| Db   | 375  | TTTAGTTTTTACCTATACCTATGTGAAGACTCTATTATGGAACCCCAATGGACATATGGGT   | 434 |            |                   |
|  |      |   |     |            |                   |
| QY   | 121  | TTGCACTCACACTTTTTTTTTTTTTTTTTTTTGTCTCGTGTATCTCAATGGGGTGGCAACAAT | 180 |            |                   |
|  |      |   |     |            |                   |
| Db   | 435  | TTGCACTCACACTTTTTTTTTTTTTTTTTTTTGTCTCGTGTATCTCAATGGGGTGGCAACAAT | 494 |            |                   |
|  |      |   |     |            |                   |

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Query Match      100.0%; Score 501; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. NO. 8.5e-13;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|                              |               |  |       |              |
|------------------------------|---------------|--|-------|--------------|
| Query Match                  | 100.0%;       | Score 501;   | DB 9; | Length 2894; |
| Best Local Similarity        | 100.0%;       | Pred. No. 8.5e-135;  |       |              |
| Matches 501; Conservative 0; | Mismatches 0; | Indels 0;  | Gaps  |              |
| QY                           | 1             | TTACAGGGCAGTGCCTTTGTAGCCTATCTCTTGATGGCTCTCAAGTCAAAAGACTTGA     | 60    |              |
|                              |               |  |       |              |
| Db                           | 315           | TTACAGGGCAGTGCCTTTGTAGCCTATCTCTTGATGGCTCTCAAGTCAAAAGACTTGA     | 374   |              |
| QY                           | 61            | TTTAGTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCCAATGACATATGGT     | 120   |              |
|                              |               |  |       |              |
| Db                           | 375           | TTTAGTTTTTACCTATACCTATGTGAAACTCTATTATGGAACCCCAATGACATATGGT     | 434   |              |
| QY                           | 121           | TTGAACCTCACACTTTTTTTTTTTTTTTTGTTCCTGTGATTCTTCATTTGGGGTGCACAAAT | 180   |              |
|                              |               |  |       |              |
| Db                           | 435           | TTGAACCTCACACTTTTTTTTTTTTTTTTGTTCCTGTGATTCTTCATTTGGGGTGCACAAAT | 494   |              |
| QY                           | 181           | AATTCATCAAGTAATCATGCCGAGGATTATTGATCAAAATCAAAAGGTAATGCACATCC    | 240   |              |



Db 495 AATTCACTAAGTAATCATGGCCAGGATATTGATCAAAATCAAAAGTAATGCACATCC 554  
QY 241 TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTCCCGGTGACACATCCATTGCTG 300  
Db 555 TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTCCCGGTGACACATCCATTGCTG 614  
QY 301 GCAATGAGTGTCCAGAGATTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360  
Db 615 GCAATGAGTGTCCAGAGATTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 674  
QY 361 GTGTCACTGCTCACTTTTGTGAAGTGTCTCTCAGAGTCTATCAACATTTGAATATCAG 420  
Db 675 GTGTCACTGCTCACTTTTGTGAAGTGTCTCTCAGAGTCTATCAACATTTGAATATCAG 734  
QY 421 TTGACAGAAATGTCGATGCGTGGTCAACATCCCTGTTGATTCCTCTGATTAAGCTGTT 480  
Db 735 TTGACAGAAATGTCGATGCGTGGTCAACATCCCTGTTGATTCCTCTGATTAAGCTGTT 794  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 795 CTGGTGGCAGTAACATGCAAC 815

RESULT 8  
US-09-984-827-22  
; Sequence 22, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (374)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-22

Query Match 100.0%; Score 501; DB 9; Length 5352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-134; Indels 0; Gaps 0;  
Matches 501; Conservative 0; Mismatches 0;  
QY 1 TTACAGGGGCGAGTCCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA 60  
Db 509 TTACAGGGGCGAGTCCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA 568  
QY 61 TTATAGTTTTTACCTATACCTATGTGAACTCTATTATGGAACCCCAATGGACATATGGGT 120  
Db 569 TTATAGTTTTTACCTATACCTATGTGAACTCTATTATGGAACCCCAATGGACATATGGGT 628  
QY 121 TTGAACATCACACTTTTTTTTTTTTTTTGTTCCCTGTGATTCCTCATTTGGGGTTGCAACAAT 180  
Db 629 TTGAACATCACACTTTTTTTTTTTTTTTGTTCCCTGTGATTCCTCATTTGGGGTTGCAACAAT 688  
QY 181 AATTCATCAAGTAATCATGCGCAGGATATTGATCAAAATCAAAAGTAATGCACATCC 240

Db 689 AATTCACTAAGTAATCATGGCCAGGATATTGATCAAAATCAAAAGTAATGCACATCC 748  
QY 241 TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTCCCGGTGACACATCCATTGCTG 300  
Db 749 TCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTCCCGGTGACACATCCATTGCTG 808  
QY 301 GCAATGAGTGTCCAGAGATTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360  
Db 809 GCAATGAGTGTCCAGAGATTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 868  
QY 361 GTGTCACTGCTCACTTTTGTGAAGTGTCTCTCAGAGTCTATCAACATTTGAATATCAG 420  
Db 869 GTGTCACTGCTCACTTTTGTGAAGTGTCTCTCAGAGTCTATCAACATTTGAATATCAG 928  
QY 421 TTGACAGAAATGTCGATGCGTGGTCAACATCCCTGTTGATTCCTCTGATTAAGCTGTT 480  
Db 929 TTGACAGAAATGTCGATGCGTGGTCAACATCCCTGTTGATTCCTCTGATTAAGCTGTT 988  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 989 CTGGTGGCAGTAACATGCAAC 1009

RESULT 9  
US-09-984-827-1  
; Sequence 1, Application US/09984827  
; Publication No. US20030056234A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFELE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 9741  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7009)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-1

Query Match 100.0%; Score 501; DB 9; Length 9741;  
Best Local Similarity 100.0%; Pred. No. 1.6e-134; Indels 0; Gaps 0;  
Matches 501; Conservative 0; Mismatches 0;  
QY 1 TTACAGGGGCGAGTCCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA 60  
Db 7144 TTACAGGGGCGAGTCCCTTTGTAGCCTATGCTCTGTATGGCTCTCAAGTGAAGACTTGAA 7203  
QY 61 TTATAGTTTTTACCTATACCTATGTGAACTCTATTATGGAACCCCAATGGACATATGGGT 120  
Db 7204 TTATAGTTTTTACCTATACCTATGTGAACTCTATTATGGAACCCCAATGGACATATGGGT 7263  
QY 121 TTGAACATCACACTTTTTTTTTTTTTTTGTTCCCTGTATTCCTCATTTGGGGTTGCAACAAT 180  
Db 7264 TTGAACATCACACTTTTTTTTTTTTTTTGTTCCCTGTATTCCTCATTTGGGGTTGCAACAAT 7323  
QY 181 AATTCATCAAGTAATCATGCGCAGGATATTGATCAAAATCAAAAGTAATGCACATCC 240  
Db 7324 AATTCATCAAGTAATCATGCGCAGGATATTGATCAAAATCAAAAGTAATGCACATCC 7383

QY 241 TCATTCACCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGGTG 300  
Db 7384 TCATTCACCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGGTG 7443  
QY 301 GCAATGAGTGTGCCAGAGTTATTAGTGCCCAAGTTTTTCAGAAAAGTTTGAAGCACCATTGGT 360  
Db 7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCCAAGTTTTTCAGAAAAGTTTGAAGCACCATTGGT 7503  
QY 361 GTGTCATGCTCAGTTTGTGAAGTGTCTGCTCAGAGTCTATCAACATTGAATATCAG 420  
Db 7504 GTGTCATGCTCAGTTTGTGAAGTGTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563  
QY 421 TTGACAGAAATGGTGGCCTGGCTTAACATCCTGCTTTGATTCCCTCGATGAAGCTGTT 480  
Db 7564 TTGACAGAAATGGTGGCCTGGCTTAACATCCTGCTTTGATTCCCTCGATGAAGCTGTT 7623  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 7624 CTGGTGGCAGTAACATGCAAC 7644

RESULT 10  
US-09-846-456-10  
; Sequence 10, Application US/09846456  
; Patent No. US20020146792A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosier, Marie  
; APPLICANT: Prades, Catherine  
; APPLICANT: Lemoine, Cendrine  
; APPLICANT: Naudin, Laurent  
; APPLICANT: Deneffe, Patrice  
; APPLICANT: Duverger, Nicolas  
; APPLICANT: Brewer, Bryan  
; APPLICANT: Remaley, Alan  
; APPLICANT: Fojo, Silvia  
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying It  
; TITLE OF INVENTION: Activity and Therapeutic Uses  
; FILE REFERENCE: 3806.0505  
; CURRENT APPLICATION NUMBER: US/09/846.456  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,280  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 9741  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: "n" is chosen from g, a, t and c  
US-09-846-456-10

Query Match 100.0%; Score 501; DB 10; Length 9741;  
Best Local Similarity 100.0%; Pred. No. 1.6e-134;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTACAGGGCAGTGCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGA 60  
Db 7144 TTACAGGGCAGTGCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGA 7203  
QY 61 TTTAGTTTTTACCTATACCTATGTAACCTCTATTATGGAACCCCAATGACATATGGT 120  
Db 7204 TTTAGTTTTTACCTATACCTATGTAACCTCTATTATGGAACCCCAATGACATATGGT 7263  
QY 121 TTGAACCTACACTTTTTTTTTTTTTTTTTTTTGTCTGTGATCTCATTCGGGTGCAACAAT 180  
Db 7264 TTGAACCTACACTTTTTTTTTTTTTTTTTTTTGTCTGTGATCTCATTCGGGTGCAACAAT 7323  
QY 181 AATTCACTAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGGTAATGCATCC 240  
Db 7324 AATTCACTAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGGTAATGCATCC 7383

QY 241 TCATTCACCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGGTG 300  
Db 7384 TCATTCACCTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATTGGTG 7443  
QY 301 GCAATGAGTGTGCCAGAGTTATTAGTGCCCAAGTTTTTCAGAAAAGTTTGAAGCACCATTGGT 360  
Db 7444 GCAATGAGTGTGCCAGAGTTATTAGTGCCCAAGTTTTTCAGAAAAGTTTGAAGCACCATTGGT 7503  
QY 361 GTGTCATGCTCAGTTTGTGAAGTGTCTGCTCAGAGTCTATCAACATTGAATATCAG 420  
Db 7504 GTGTCATGCTCAGTTTGTGAAGTGTCTGCTCAGAGTCTATCAACATTGAATATCAG 7563  
QY 421 TTGACAGAAATGGTGGCCTGGCTTAACATCCTGCTTTGATTCCCTCGATGAAGCTGTT 480  
Db 7564 TTGACAGAAATGGTGGCCTGGCTTAACATCCTGCTTTGATTCCCTCGATGAAGCTGTT 7623  
QY 481 CTGGTGGCAGTAACATGCAAC 501  
Db 7624 CTGGTGGCAGTAACATGCAAC 7644

RESULT 11  
US-09-984-827-92  
; Sequence 92, Application US/09984827  
; Publication No. US2003005623A1  
; GENERAL INFORMATION:  
; APPLICANT: DENEFFE, PATRICE  
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE  
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE  
; APPLICANT: DUVERGER, NICOLAS  
; APPLICANT: CAMBIEN, FRANCOIS  
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABC1 GENE, THEIR USES, AND  
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR  
; FILE REFERENCE: 03806.0522-00000  
; CURRENT APPLICATION NUMBER: US/09/984,827  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: 60/254,108  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: FR 00/14037  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 92  
; LENGTH: 9870  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (7138)  
; OTHER INFORMATION: a, t, c or g  
US-09-984-827-92

Query Match 100.0%; Score 501; DB 9; Length 9870;  
Best Local Similarity 100.0%; Pred. No. 1.6e-134;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTACAGGGCAGTGCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGA 60  
Db 7273 TTACAGGGCAGTGCCTTTGTAGCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGA 7332  
QY 61 TTTAGTTTTTACCTATACCTATGTAACCTCTATTATGGAACCCCAATGACATATGGT 120  
Db 7333 TTTAGTTTTTACCTATACCTATGTAACCTCTATTATGGAACCCCAATGACATATGGT 7392  
QY 121 TTGAACCTACACTTTTTTTTTTTTTTTTTTTTGTCTGTGATCTCATTCGGGTGCAACAAT 180  
Db 7393 TTGAACCTACACTTTTTTTTTTTTTTTTTTTTGTCTGTGATCTCATTCGGGTGCAACAAT 7452  
QY 181 AATTCACTAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGGTAATGCATCC 240  
Db 7453 AATTCACTAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGGTAATGCATCC 7512



Db 7513 TCATTCACTAAGCCATGCCATGCCAGAGACTGGTTCCGGTGACACATCCATTGCTG 7572

QY 301 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGGT 360

Db 7573 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGGT 7632

QY 361 GTGTCATGCTCACTTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG 420

Db 7633 GTGTCATGCTCACTTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG 7692

QY 421 TTGACAGAATGGTCCATGGCTGGCTAAACATCTGTTTGAATTCCTCTGATAAGCTGTT 480

Db 7693 TTGACAGAATGGTCCATGGCTGGCTAAACATCTGTTTGAATTCCTCTGATAAGCTGTT 7752

QY 481 CTGGTGGCAGTAACATGCAAC 501

Db 7753 CTGGTGGCAGTAACATGCAAC 7773

## RESULT 14

US-09-984-827-96

; Sequence 95, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFELE, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984,827

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: FR 00/14037

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 95

; LENGTH: 9870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7138)

; OTHER INFORMATION: a, t, c or g

US-09-984-827-95

Query Match 100.0%; Score 501; DB 9; Length 9870;

Best Local Similarity 100.0%; Pred. No. 1.6e-134;

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGGCTTTGTAGCCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 60

Db 7273 TTACAGGGCAGTGGCTTTGTAGCCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 7332

QY 61 TTAGTTTTTACCTATACCTATGTAAGAACTCTATTATGGAACCAATGGACATATGGT 120

Db 7333 TTAGTTTTTACCTATACCTATGTAAGAACTCTATTATGGAACCAATGGACATATGGT 7392

QY 121 TTGAACACACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGCTGATTCCTATGGGGTTGCAACAAT 180

Db 7393 TTGAACACACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGCTGATTCCTATGGGGTTGCAACAAT 7452

QY 181 AATTCATCAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGTAATGCATCC 240

Db 7453 AATTCATCAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGTAATGCATCC 7512

QY 241 TCATTCAATAGCCATGCCATGCCAGAGACTGGTTCCCGGTGACATCCATTGCTG 300

Db 7513 TCATTCAATAGCCATGCCATGCCAGAGACTGGTTCCCGGTGACATCCATTGCTG 7572

QY 301 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGGT 360

Db 7573 GCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCACCATTGGT 7632

QY 361 GTGTCATGCTCACTTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG 420

Db 7633 GTGTCATGCTCACTTTTGTGAAGCTGCTCTGCTCAGAGTCTATCAACATTTGAATATCAG 7692

QY 421 TTGACAGAATGGTCCATGGCTGGCTAAACATCTGTTTGAATTCCTCTGATAAGCTGTT 480

Db 7693 TTGACAGAATGGTCCATGGCTGGCTAAACATCTGTTTGAATTCCTCTGATAAGCTGTT 7752

QY 481 CTGGTGGCAGTAACATGCAAC 501

Db 7753 CTGGTGGCAGTAACATGCAAC 7773

## RESULT 15

US-09-984-827-96

; Sequence 96, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFELE, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984,827

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: FR 00/14037

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 96

; LENGTH: 9870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (7138)

; OTHER INFORMATION: a, t, c or g

US-09-984-827-96

Query Match 100.0%; Score 501; DB 9; Length 9870;

Best Local Similarity 100.0%; Pred. No. 1.6e-134;

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACAGGGCAGTGGCTTTGTAGCCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 60

Db 7273 TTACAGGGCAGTGGCTTTGTAGCCCTATGCTTGTATGGCTCTCAAGTGAAGACTTGAA 7332

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QY 121 TTGAACACACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGCTGATTCCTATGGGGTTGCAACAAT 180

Db 7393 TTGAACACACTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGCTGATTCCTATGGGGTTGCAACAAT 7452

QY 181 AATTCATCAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGTAATGCATCC 240

Db 7453 AATTCATCAAGTAATCATGGCCAGGATTTATGATCAAAATCAAAAGTAATGCATCC 7512

QY 241 TCATTCAATAGCCATGCCATGCCAGAGACTGGTTCCCGGTGACATCCATTGCTG 300

Db 7513 TCATTCAATAGCCATGCCATGCCAGAGACTGGTTCCCGGTGACATCCATTGCTG 7572